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FIG.1A

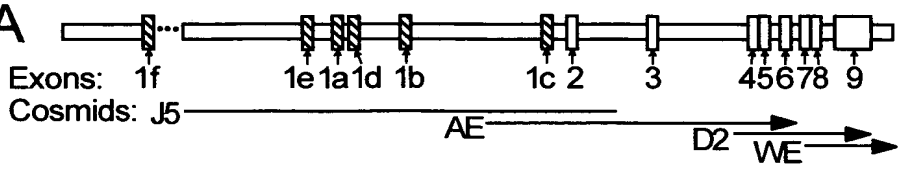

FIG.1B

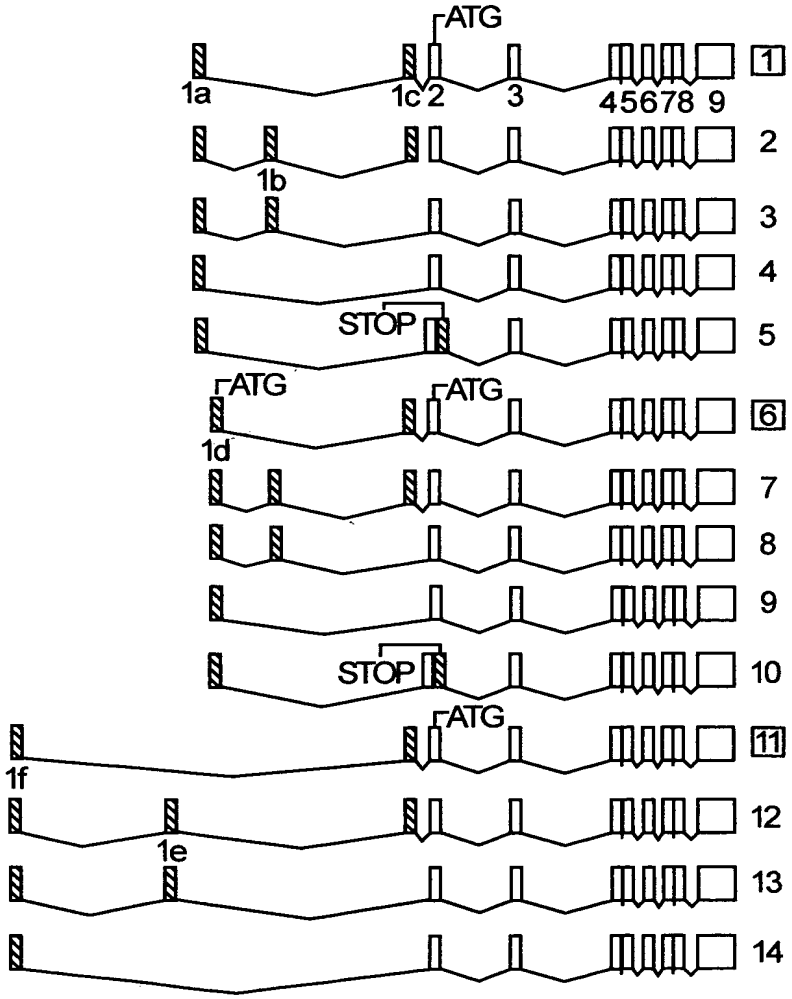

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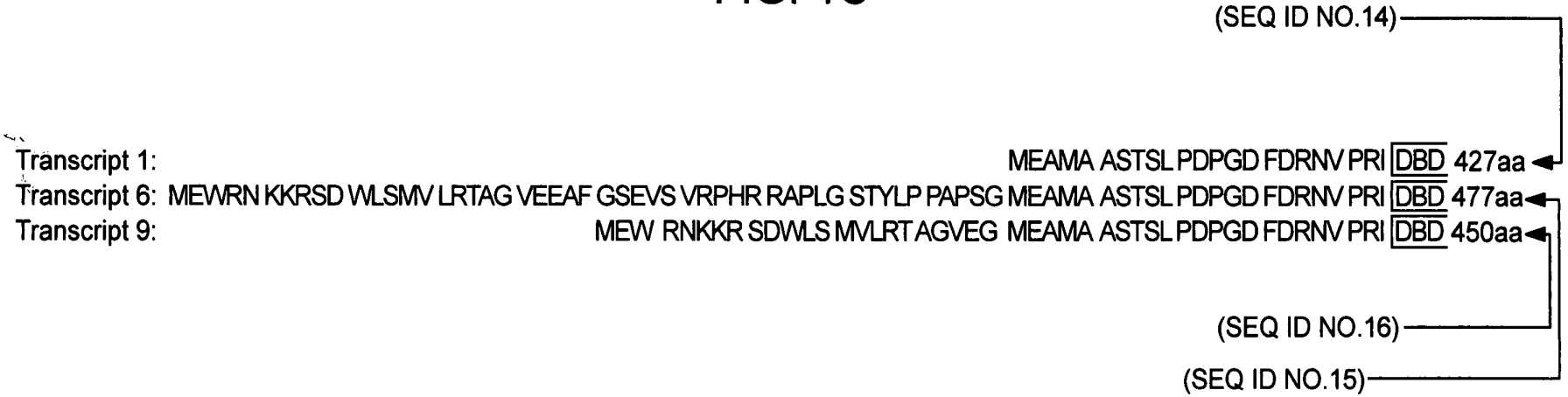
FIG. 1C



Title: "Isoforms of the Human Vitamin D Receptor"
Inventor: Linda Anne Crofts
Application No.: 09/509,482
Atty. Docket No. RICE-014

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FIG. 4

A. 5'...atcccttaag GGCTCCTGAACCTAGCCCAGCTGGACGGAG
AAATGGACTCTAGCCTCCTCTGATAGCCTCATGCCAGGCCC
CGTGCACATTGCTTTGCTTGCCTCCCTCAATCCTCATAGCT
TCTCTTTGGGgtaagtacag...3' (SEQ ID NO: 13)

B. 5'...TGCGACCTTGGCGGTGAGCCTGGGGACAGGGGTGAGGC
CAGAGACGGACGGACGCAGGGGCCCGGCCCAAGGCGAGGG
AGAACAGCGGCACTAAGGCAGAAAGGAAGAGGGCGGTGTG
TTCACCCGCAGCCCAATCCATCACTCAGCAACTCCTAGAC
GCTGGTAGAAAGTTCCTCCGAGGAGCCTGCCATCCAGTCGT
GCGTGCAG...3' (SEQ ID NO: 5)

C. 5'...tgtttttag AGGCAGCATGAAACAGTGGGATGTGCAGAG
AGAAGATCTGGGTCCAGTAGCTCTGACACTCCTCAGCTGT
AGAAACCTTGACAACTCTGCACATCAGTTGTACAATGGAA
CGGTATTTTTTACTCTTCATGTCTGAAAAGGCTATGATAA
AGATCAAgtaagatatt...3' (SEQ ID NO: 6)

D. 5'...GTTTCCTTCTTCTGTCGGGGCGCCTTGGCATGGAGTGG
AGGAATAAGAAAAGGAGCGATTGGCTGTCGATGGTGCTCA
GAACTGCTGGAGTGGAGGgtgtgtaacc...3' (SEQ ID NO: 1)

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FIG. 5A

Transcript 6
(Sequence Range: 1 to 1463)

```
        10          20          30          40          50
     *   *   *   *   *   *   *   *   *   *
GTTTCCTTCT TCTGTCGGGG CGCCTTGGCA TGGAGTGGAG GAATAAGAAA
CAAAGGAAGA AGACAGCCCC GCGGAACCGT ACCTCACCTC CTTATTCTTT
                                  MetGluTrpArg AsnLysLys>

        60          70          80          90          100
     *   *   *   *   *   *   *   *   *   *
AGGAGCGATT GGCTGTCGAT GGTGCTCAGA ACTGCTGGAG TGGAGGAAGC
TCCTCGCTAA CCGACAGCTA CCACGAGTCT TGACGACCTC ACCTCCTTCG
ArgSerAsp TrpLeuSerMet ValLeuArg ThrAlaGly ValGluGluAla>

       110         120         130         140         150
     *   *   *   *   *   *   *   *   *   *
CTTTGGGTCT GAAGTGTCTG TGAGACCTCA CAGAAGAGCA CCCCTGGGCT
GAAACCCAGA CTTCACAGAC ACTCTGGAGT GTCTTCTCGT GGGGACCCGA
 PheGlySer GluValSer ValArgProHis ArgArgAla ProLeuGly>

       160         170         180         190         200
     *   *   *   *   *   *   *   *   *   *
CCACTTACCT GCCCCCTGCT CCTTCAGGGA TGGAGGCAAT GGCGGCCAGC
GGTGAATGGA CGGGGGACGA GGAAGTCCCT ACCTCCGTTA CCGCCGGTCG
SerThrTyrLeu ProProAla ProSerGly MetGluAlaMet AlaAlaSer>

       210         220         230         240         250
     *   *   *   *   *   *   *   *   *   *
ACTTCCCTGC CTGACCCTGG AGACTTTGAC CGGAACGTGC CCCGGATCTG
TGAAGGGACG GACTGGGACC TCTGAAACTG GCCTTGCACG GGGCCTAGAC
ThrSerLeu ProAspProGly AspPheAsp ArgAsnVal ProArgIleCys>

       260         270         280         290         300
     *   *   *   *   *   *   *   *   *   *
TGGGGTGTGT GGAGACCGAG CCACTGGCTT TCACTTCAAT GCTATGACCT
ACCCCACACA CCTCTGGCTC GGTGACCGAA AGTGAAGTTA CGATACTGGA
 GlyValCys GlyAspArg AlaThrGlyPhe HisPheAsn AlaMetThr>

       310         320         330         340         350
     *   *   *   *   *   *   *   *   *   *
GTGAAGGCTG CAAAGGCTTC TTCAGGCGAA GCATGAAGCG GAAGGCACTA
CACTTCCGAC GTTTCCGAAG AAGTCCGCTT CGTACTTCGC CTTCCGTGAT
CysGluGlyCys LysGlyPhe PheArgArg SerMetLysArg LysAlaLeu>

       360         370         380         390         400
     *   *   *   *   *   *   *   *   *   *
TTCACCTGCC CCTTCAACGG GGACTGCCGC ATCACCAAGG ACAACCGACG
AAGTGGACGG GGAAGTTGCC CCTGACGGCG TAGTGGTTCC TGTTGGCTGC
PheThrCys ProPheAsnGly AspCysArg IleThrLys AspAsnArgArg>
```

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FIG. 5B

```
          410         420         430         440         450
           *   *       *   *       *   *       *   *       *   *
CCACTGCCAG GCCTGCCGGC TCAAACGCTG TGTGGACATC GGCATGATGA
GGTGACGGTC CGGACGGCCG AGTTTGCGAC ACACCTGTAG CCGTACTACT
 HisCysGln AlaCysArg LeuLysArgCys ValAspIle GlyMetMet>

          460         470         480         490         500
           *   *       *   *       *   *       *   *       *   *
AGGAGTTCAT TCTGACAGAT GAGGAAGTGC AGAGGAAGCG GGAGATGATC
TCCTCAAGTA AGACTGTCTA CTCCTTCACG TCTCCTTCGC CCTCTACTAG
LysGluPheIle LeuThrAsp GluGluVal GlnArgLysArg GluMetIle>

          510         520         530         540         550
           *   *       *   *       *   *       *   *       *   *
CTGAAGCGGA AGGAGGAGGA GGCCTTGAAG GACAGTCTGC GGCCCAAGCT
GACTTCGCCT TCCTCCTCCT CCGGAACTTC CTGTCAGACG CCGGGTTCGA
LeuLysArg LysGluGluGlu AlaLeuLys AspSerLeu ArgProLysLeu>

          560         570         580         590         600
           *   *       *   *       *   *       *   *       *   *
GTCTGAGGAG CAGCAGCGCA TCATTGCCAT ACTGCTGGAC GCCCACCATA
CAGACTCCTC GTCGTCGCGT AGTAACGGTA TGACGACCTG CGGGTGGTAT
 SerGluGlu GlnGlnArg IleIleAlaIle LeuLeuAsp AlaHisHis>

          610         620         630         640         650
           *   *       *   *       *   *       *   *       *   *
AGACCTACGA CCCCACCTAC TCCGACTTCT GCCAGTTCCG GCCTCCAGTT
TCTGGATGCT GGGGTGGATG AGGCTGAAGA CGGTCAAGGC CGGAGGTCAA
LysThrTyrAsp ProThrTyr SerAspPhe CysGlnPheArg ProProVal>

          660         670         680         690         700
           *   *       *   *       *   *       *   *       *   *
CGTGTGAATG ATGGTGGAGG GAGCCATCCT TCCAGGCCCA ACTCCAGACA
GCACACTTAC TACCACCTCC CTCGGTAGGA AGGTCCGGGT TGAGGTCTGT
ArgValAsn AspGlyGlyGly SerHisPro SerArgPro AsnSerArgHis>

          710         720         730         740         750
           *   *       *   *       *   *       *   *       *   *
CACTCCCAGC TTCTCTGGGG ACTCCTCCTC CTCCTGCTCA GATCACTGTA
GTGAGGGTCG AAGAGACCCC TGAGGAGGAG GAGGACGAGT CTAGTGACAT
 ThrProSer PheSerGly AspSerSerSer SerCysSer AspHisCys>

          760         770         780         790         800
           *   *       *   *       *   *       *   *       *   *
TCACCTCTTC AGACATGATG GACTCGTCCA GCTTCTCCAA TCTGGATCTG
AGTGGAGAAG TCTGTACTAC CTGAGCAGGT CGAAGAGGTT AGACCTAGAC
IleThrSerSer AspMetMet AspSerSer SerPheSerAsn LeuAspLeu>

          810         820         830         840         850
           *   *       *   *       *   *       *   *       *   *
AGTGAAGAAG ATTCAGATGA CCCTTCTGTG ACCCTAGAGC TGTCCCAGCT
TCACTTCTTC TAAGTCTACT GGGAAGACAC TGGGATCTCG ACAGGGTCGA
SerGluGlu AspSerAspAsp ProSerVal ThrLeuGlu LeuSerGlnLeu>
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FIG. 5C

```
      860        870        880        890        900
    *   *      *   *      *   *      *   *      *   *
CTCCATGCTG CCCCACCTGG CTGACCTGGT CAGTTACAGC ATCCAAAAGG
GAGGTACGAC GGGGTGGACC GACTGGACCA GTCAATGTCG TAGGTTTTCC
 SerMetLeu ProHisLeu AlaAspLeuVal SerTyrSer IleGlnLys>

      910        920        930        940        950
    *   *      *   *      *   *      *   *      *   *
TCATTGGCTT TGCTAAGATG ATACCAGGAT TCAGAGACCT CACCTCTGAG
AGTAACCGAA ACGATTCTAC TATGGTCCTA AGTCTCTGGA GTGGAGACTC
ValIleGlyPhe AlaLysMet IleProGly PheArgAspLeu ThrSerGlu>

      960        970        980        990       1000
    *   *      *   *      *   *      *   *      *   *
GACCAGATCG TACTGCTGAA GTCAAGTGCC ATTGAGGTCA TCATGTTGCG
CTGGTCTAGC ATGACGACTT CAGTTCACGG TAACTCCAGT AGTACAACGC
AspGlnIle ValLeuLeuLys SerSerAla IleGluVal IleMetLeuArg>

     1010       1020       1030       1040       1050
    *   *      *   *      *   *      *   *      *   *
CTCCAATGAG TCCTTCACCA TGGACGACAT GTCCTGGACC TGTGGCAACC
GAGGTTACTC AGGAAGTGGT ACCTGCTGTA CAGGACCTGG ACACCGTTGG
 SerAsnGlu SerPheThr MetAspAspMet SerTrpThr CysGlyAsn>

     1060       1070       1080       1090       1100
    *   *      *   *      *   *      *   *      *   *
AAGACTACAA GTACCGCGTC AGTGACGTGA CCAAAGCCGG ACACAGCCTG
TTCTGATGTT CATGGCGCAG TCACTGCACT GGTTTCGGCC TGTGTCGGAC
GlnAspTyrLys TyrArgVal SerAspVal ThrLysAlaGly HisSerLeu>

     1110       1120       1130       1140       1150
    *   *      *   *      *   *      *   *      *   *
GAGCTGATTG AGCCCCTCAT CAAGTTCCAG GTGGGACTGA AGAAGCTGAA
CTCGACTAAC TCGGGGAGTA GTTCAAGGTC CACCCTGACT TCTTCGACTT
GluLeuIle GluProLeuIle LysPheGln ValGlyLeu LysLysLeuAsn>

     1160       1170       1180       1190       1200
    *   *      *   *      *   *      *   *      *   *
CTTGCATGAG GAGGAGCATG TCCTGCTCAT GGCCATCTGC ATCGTCTCCC
GAACGTACTC CTCCTCGTAC AGGACGAGTA CCGGTAGACG TAGCAGAGGG
 LeuHisGlu GluGluHis ValLeuLeuMet AlaIleCys IleValSer>

     1210       1220       1230       1240       1250
    *   *      *   *      *   *      *   *      *   *
CAGATCGTCC TGGGGTGCAG GACGCCGCGC TGATTGAGGC CATCCAGGAC
GTCTAGCAGG ACCCCACGTC CTGCGGCGCG ACTAACTCCG GTAGGTCCTG
ProAspArgPro GlyValGln AspAlaAla LeuIleGluAla IleGlnAsp>

     1260       1270       1280       1290       1300
    *   *      *   *      *   *      *   *      *   *
CGCCTGTCCA ACACACTGCA GACGTACATC CGCTGCCGCC ACCCGCCCCC
GCGGACAGGT TGTGTGACGT CTGCATGTAG GCGACGGCGG TGGGCGGGGG
ArgLeuSer AsnThrLeuGln ThrTyrIle ArgCysArg HisProProPro>
```

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FIG. 5D

```
      1310        1320        1330        1340        1350
     *    *      *    *      *    *      *    *      *    *
 GGGCAGCCAC CTGCTCTATG CCAAGATGAT CCAGAAGCTA GCCGACCTGC
 CCCGTCGGTG GACGAGATAC GGTTCTACTA GGTCTTCGAT CGGCTGGACG
  GlySerHis LeuLeuTyr AlaLysMetIle GlnLysLeu AlaAspLeu>

      1360        1370        1380        1390        1400
     *    *      *    *      *    *      *    *      *    *
 GCAGCCTCAA TGAGGAGCAC TCCAAGCAGT ACCGCTGCCT CTCCTTCCAG
 CGTCGGAGTT ACTCCTCGTG AGGTTCGTCA TGGCGACGGA GAGGAAGGTC
ArgSerLeuAsn GluGluHis SerLysGln TyrArgCysLeu SerPheGln>

      1410        1420        1430        1440        1450
     *    *      *    *      *    *      *    *      *    *
 CCTGAGTGCA GCATGAAGCT AACGCCCCTT GTGCTCGAAG TGTTTGGCAA
 GGACTCACGT CGTACTTCGA TTGCGGGGAA CACGAGCTTC ACAAACCGTT
 ProGluCys SerMetLysLeu ThrProLeu ValLeuGlu ValPheGlyAsn>

      1460
     *    *
 TGAGATCTCC TGA (SEQ ID NO:2)
 ACTCTAGAGG ACT (SEQ ID NO:17)
  GluIleSer ***>(SEQ ID NO:9)
```

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FIG. 6A

Transcript 9
(Sequence range: 1 to 1382)

```
        10          20          30          40          50
    *   *   *   *   *   *   *   *   *   *   *   *   *   *
GTTTCCTTCT TCTGTCGGGG CGCCTTGGCA TGGAGTGGAG GAATAAGAAA
CAAAGGAAGA AGACAGCCCC GCGGAACCGT ACCTCACCTC CTTATTCTTT
                                 MetGluTrpArg AsnLysLys>

        60          70          80          90          100
    *   *   *   *   *   *   *   *   *   *   *   *   *   *
AGGAGCGATT GGCTGTCGAT GGTGCTCAGA ACTGCTGGAG TGGAGGGGAT
TCCTCGCTAA CCGACAGCTA CCACGAGTCT TGACGACCTC ACCTCCCCTA
ArgSerAsp TrpLeuSerMet ValLeuArg ThrAlaGly ValGluGlyMet>

        110         120         130         140         150
    *   *   *   *   *   *   *   *   *   *   *   *   *   *
GGAGGCAATG GCGGCCAGCA CTTCCCTGCC TGACCCTGGA GACTTTGACC
CCTCCGTTAC CGCCGGTCGT GAAGGGACGG ACTGGGACCT CTGAAACTGG
 GluAlaMet AlaAlaSer ThrSerLeuPro AspProGly AspPheAsp>

        160         170         180         190         200
    *   *   *   *   *   *   *   *   *   *   *   *   *   *
GGAACGTGCC CCGGATCTGT GGGGTGTGTG GAGACCGAGC CACTGGCTTT
CCTTGCACGG GGCCTAGACA CCCCACACAC CTCTGGCTCG GTGACCGAAA
ArgAsnValPro ArgIleCys GlyValCys GlyAspArgAla ThrGlyPhe>

        210         220         230         240         250
    *   *   *   *   *   *   *   *   *   *   *   *   *   *
CACTTCAATG CTATGACCTG TGAAGGCTGC AAAGGCTTCT TCAGGCGAAG
GTGAAGTTAC GATACTGGAC ACTTCCGACG TTTCCGAAGA AGTCCGCTTC
HisPheAsn AlaMetThrCys GluGlyCys LysGlyPhe PheArgArgSer>

        260         270         280         290         300
    *   *   *   *   *   *   *   *   *   *   *   *   *   *
CATGAAGCGG AAGGCACTAT TCACCTGCCC CTTCAACGGG GACTGCCGCA
GTACTTCGCC TTCCGTGATA AGTGGACGGG GAAGTTGCCC CTGACGGCGT
 MetLysArg LysAlaLeu PheThrCysPro PheAsnGly AspCysArg>

        310         320         330         340         350
    *   *   *   *   *   *   *   *   *   *   *   *   *   *
TCACCAAGGA CAACCGACGC CACTGCCAGG CCTGCCGGCT CAAACGCTGT
AGTGGTTCCT GTTGGCTGCG GTGACGGTCC GGACGGCCGA GTTTGCGACA
IleThrLysAsp AsnArgArg HisCysGln AlaCysArgLeu LysArgCys>

        360         370         380         390         400
    *   *   *   *   *   *   *   *   *   *   *   *   *   *
GTGGACATCG GCATGATGAA GGAGTTCATT CTGACAGATG AGGAAGTGCA
CACCTGTAGC CGTACTACTT CCTCAAGTAA GACTGTCTAC TCCTTCACGT
ValAspIle GlyMetMetLys GluPheIle LeuThrAsp GluGluValGln>
```

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FIG. 6B

```
                410       420       430       440       450
                 *  *      *  *      *  *      *  *      *  *
GAGGAAGCGG GAGATGATCC TGAAGCGGAA GGAGGAGGAG GCCTTGAAGG
CTCCTTCGCC CTCTACTAGG ACTTCGCCTT CCTCCTCCTC CGGAACTTCC
 ArgLysArg GluMetIle LeuLysArgLys GluGluGlu AlaLeuLys>

                460       470       480       490       500
                 *  *      *  *      *  *      *  *      *  *
 ACAGTCTGCG GCCCAAGCTG TCTGAGGAGC AGCAGCGCAT CATTGCCATA
 TGTCAGACGC CGGGTTCGAC AGACTCCTCG TCGTCGCGTA GTAACGGTAT
AspSerLeuArg ProLysLeu SerGluGlu GlnGlnArgIle IleAlaIle>

                510       520       530       540       550
                 *  *      *  *      *  *      *  *      *  *
CTGCTGGACG CCCACCATAA GACCTACGAC CCCACCTACT CCGACTTCTG
GACGACCTGC GGGTGGTATT CTGGATGCTG GGGTGGATGA GGCTGAAGAC
LeuLeuAsp AlaHisHisLys ThrTyrAsp ProThrTyr SerAspPheCys>

                560       570       580       590       600
                 *  *      *  *      *  *      *  *      *  *
CCAGTTCCGG CCTCCAGTTC GTGTGAATGA TGGTGGAGGG AGCCATCCTT
GGTCAAGGCC GGAGGTCAAG CACACTTACT ACCACCTCCC TCGGTAGGAA
 GlnPheArg ProProVal ArgValAsnAsp GlyGlyGly SerHisPro>

                610       620       630       640       650
                 *  *      *  *      *  *      *  *      *  *
 CCAGGCCCAA CTCCAGACAC ACTCCCAGCT TCTCTGGGGA CTCCTCCTCC
 GGTCCGGGTT GAGGTCTGTG TGAGGGTCGA AGAGACCCCT GAGGAGGAGG
SerArgProAsn SerArgHis ThrProSer PheSerGlyAsp SerSerSer>

                660       670       680       690       700
                 *  *      *  *      *  *      *  *      *  *
 TCCTGCTCAG ATCACTGTAT CACCTCTTCA GACATGATGG ACTCGTCCAG
 AGGACGAGTC TAGTGACATA GTGGAGAAGT CTGTACTACC TGAGCAGGTC
 SerCysSer AspHisCysIle ThrSerSer AspMetMet AspSerSerSer>

                710       720       730       740       750
                 *  *      *  *      *  *      *  *      *  *
  CTTCTCCAAT CTGGATCTGA GTGAAGAAGA TTCAGATGAC CCTTCTGTGA
  GAAGAGGTTA GACCTAGACT CACTTCTTCT AAGTCTACTG GGAAGACACT
   PheSerAsn LeuAspLeu SerGluGluAsp SerAspAsp ProSerVal>

                760       770       780       790       800
                 *  *      *  *      *  *      *  *      *  *
  CCCTAGAGCT GTCCCAGCTC TCCATGCTGC CCCACCTGGC TGACCTGGTC
  GGGATCTCGA CAGGGTCGAG AGGTACGACG GGGTGGACCG ACTGGACCAG
  ThrLeuGluLeu SerGlnLeu SerMetLeu ProHisLeuAla AspLeuVal>

                810       820       830       840       850
                 *  *      *  *      *  *      *  *      *  *
   AGTTACAGCA TCCAAAAGGT CATTGGCTTT GCTAAGATGA TACCAGGATT
   TCAATGTCGT AGGTTTTCCA GTAACCGAAA CGATTCTACT ATGGTCCTAA
   SerTyrSer IleGlnLysVal IleGlyPhe AlaLysMet IleProGlyPhe>
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FIG. 6C

```
          860       870       880       890       900
      *    *    *    *    *    *    *    *    *    *
CAGAGACCTC ACCTCTGAGG ACCAGATCGT ACTGCTGAAG TCAAGTGCCA
GTCTCTGGAG TGGAGACTCC TGGTCTAGCA TGACGACTTC AGTTCACGGT
 ArgAspLeu ThrSerGlu AspGlnIleVal LeuLeuLys SerSerAla>

          910       920       930       940       950
      *    *    *    *    *    *    *    *    *    *
TTGAGGTCAT CATGTTGCGC TCCAATGAGT CCTTCACCAT GGACGACATG
AACTCCAGTA GTACAACGCG AGGTTACTCA GGAAGTGGTA CCTGCTGTAC
IleGluValIle MetLeuArg SerAsnGlu SerPheThrMet AspAspMet>

          960       970       980       990      1000
      *    *    *    *    *    *    *    *    *    *
TCCTGGACCT GTGGCAACCA AGACTACAAG TACCGCGTCA GTGACGTGAC
AGGACCTGGA CACCGTTGGT TCTGATGTTC ATGGCGCAGT CACTGCACTG
SerTrpThr CysGlyAsnGln AspTyrLys TyrArgVal SerAspValThr>

         1010      1020      1030      1040      1050
      *    *    *    *    *    *    *    *    *    *
CAAAGCCGGA CACAGCCTGG AGCTGATTGA GCCCCTCATC AAGTTCCAGG
GTTTCGGCCT GTGTCGGACC TCGACTAACT CGGGGAGTAG TTCAAGGTCC
 LysAlaGly HisSerLeu GluLeuIleGlu ProLeuIle LysPheGln>

         1060      1070      1080      1090      1100
      *    *    *    *    *    *    *    *    *    *
TGGGACTGAA GAAGCTGAAC TTGCATGAGG AGGAGCATGT CCTGCTCATG
ACCCTGACTT CTTCGACTTG AACGTACTCC TCCTCGTACA GGACGAGTAC
ValGlyLeuLys LysLeuAsn LeuHisGlu GluGluHisVal LeuLeuMet>

         1110      1120      1130      1140      1150
      *    *    *    *    *    *    *    *    *    *
GCCATCTGCA TCGTCTCCCC AGATCGTCCT GGGGTGCAGG ACGCCGCGCT
CGGTAGACGT AGCAGAGGGG TCTAGCAGGA CCCCACGTCC TGCGGCGCGA
AlaIleCys IleValSerPro AspArgPro GlyValGln AspAlaAlaLeu>

         1160      1170      1180      1190      1200
      *    *    *    *    *    *    *    *    *    *
GATTGAGGCC ATCCAGGACC GCCTGTCCAA CACACTGCAG ACGTACATCC
CTAACTCCGG TAGGTCCTGG CGGACAGGTT GTGTGACGTC TGCATGTAGG
 IleGluAla IleGlnAsp ArgLeuSerAsn ThrLeuGln ThrTyrIle>

         1210      1220      1230      1240      1250
      *    *    *    *    *    *    *    *    *    *
GCTGCCGCCA CCCGCCCCCG GGCAGCCACC TGCTCTATGC CAAGATGATC
CGACGGCGGT GGGCGGGGGC CCGTCGGTGG ACGAGATACG GTTCTACTAG
ArgCysArgHis ProProPro GlySerHis LeuLeuTyrAla LysMetIle>

         1260      1270      1280      1290      1300
      *    *    *    *    *    *    *    *    *    *
CAGAAGCTAG CCGACCTGCG CAGCCTCAAT GAGGAGCACT CCAAGCAGTA
GTCTTCGATC GGCTGGACGC GTCGGAGTTA CTCCTCGTGA GGTTCGTCAT
GlnLysLeu AlaAspLeuArg SerLeuAsn GluGluHis SerLysGlnTyr>
```

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FIG. 6D

```
      1310        1320        1330        1340        1350
    *    *      *    *      *    *      *    *      *    *
CCGCTGCCTC TCCTTCCAGC CTGAGTGCAG CATGAAGCTA ACGCCCCTTG
GGCGACGGAG AGGAAGGTCG GACTCACGTC GTACTTCGAT TGCGGGGAAC
 ArgCysLeu SerPheGln ProGluCysSer MetLysLeu ThrProLeu>

      1360        1370        1380
    *    *      *    *      *    *
TGCTCGAAGT GTTTGGCAAT GAGATCTCCT GA  (SEQ ID NO:3)
ACGAGCTTCA CAAACCGTTA CTCTAGAGGA CT  (SEQ ID NO:18)
ValLeuGluVal PheGlyAsn GluIleSer ***>  (SEQ ID NO:10)
```

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FIG. 7A

Transcript 10
(Sequence Range: 1 to 1534)

```
        10         20         30         40         50
    *    *     *    *     *    *     *    *     *    *
GTTTCCTTCT TCTGTCGGGG CGCCTTGGCA TGGAGTGGAG GAATAAGAAA
CAAAGGAAGA AGACAGCCCC GCGGAACCGT ACCTCACCTC CTTATTCTTT
                                  MetGluTrpArg AsnLysLys>

        60         70         80         90        100
    *    *     *    *     *    *     *    *     *    *
AGGAGCGATT GGCTGTCGAT GGTGCTCAGA ACTGCTGGAG TGGAGGGGAT
TCCTCGCTAA CCGACAGCTA CCACGAGTCT TGACGACCTC ACCTCCCCTA
ArgSerAsp TrpLeuSerMet ValLeuArg ThrAlaGly ValGluGlyMet>

       110        120        130        140        150
    *    *     *    *     *    *     *    *     *    *
GGAGGCAATG GCGGCCAGCA CTTCCCTGCC TGACCCTGGA GACTTTGACC
CCTCCGTTAC CGCCGGTCGT GAAGGGACGG ACTGGGACCT CTGAAACTGG
 GluAlaMet AlaAlaSer ThrSerLeuPro AspProGly AspPheAsp>

       160        170        180        190        200
    *    *     *    *     *    *     *    *     *    *
GGAACGTGCC CCGGATCTGT GGGGTGTGTG GAGACCGAGC CACTGGCTTT
CCTTGCACGG GGCCTAGACA CCCCACACAC CTCTGGCTCG GTGACCGAAA
ArgAsnValPro ArgIleCys GlyValCys GlyAspArgAla ThrGlyPhe>

       210        220        230        240        250
    *    *     *    *     *    *     *    *     *    *
CACTTCAATG CTATGACCTG TGAAGGCTGC AAAGGCTTCT TCAGGTGAGC
GTGAAGTTAC GATACTGGAC ACTTCCGACG TTTCCGAAGA AGTCCACTCG
HisPheAsn AlaMetThrCys GluGlyCys LysGlyPhe PheArg***(SEQ ID NO:11)

       260        270        280        290        300
    *    *     *    *     *    *     *    *     *    *
CCCCCTCCCA GGCTCTCCCC AGTGGAAAGG GAGGGAGAAG AAGCAAGGTG
GGGGGAGGGT CCGAGAGGGG TCACCTTTCC CTCCCTCTTC TTCGTTCCAC

       310        320        330        340        350
    *    *     *    *     *    *     *    *     *    *
TTTCCATGAA GGGAGCCCTT GCATTTTTCA CATCTCCTTC CTTACAATGT
AAAGGTACTT CCCTCGGGAA CGTAAAAAGT GTAGAGGAAG GAATGTTACA

       360        370        380        390        400
    *    *     *    *     *    *     *    *     *    *
CCATGGAACA TGCGGCGCTC ACAGCCACAG GAGCAGGAGG GTCTTGGCGA
GGTACCTTGT ACGCCGCGAG TGTCGGTGTC CTCGTCCTCC CAGAACCGCT
```

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FIG. 7B

```
      410         420         430         440         450
    *   *       *   *       *   *       *   *       *   *
AGCATGAAGC GGAAGGCACT ATTCACCTGC CCCTTCAACG GGGACTGCCG
TCGTACTTCG CCTTCCGTGA TAAGTGGACG GGGAAGTTGC CCCTGACGGC

      460         470         480         490         500
    *   *       *   *       *   *       *   *       *   *
CATCACCAAG GACAACCGAC GCCACTGCCA GGCCTGCCGG CTCAAACGCT
GTAGTGGTTC CTGTTGGCTG CGGTGACGGT CCGGACGGCC GAGTTTGCGA

      510         520         530         540         550
    *   *       *   *       *   *       *   *       *   *
GTGTGGACAT CGGCATGATG AAGGAGTTCA TTCTGACAGA TGAGGAAGTG
CACACCTGTA GCCGTACTAC TTCCTCAAGT AAGACTGTCT ACTCCTTCAC

      560         570         580         590         600
    *   *       *   *       *   *       *   *       *   *
CAGAGGAAGC GGGAGATGAT CCTGAAGCGG AAGGAGGAGG AGGCCTTGAA
GTCTCCTTCG CCCTCTACTA GGACTTCGCC TTCCTCCTCC TCCGGAACTT

      610         620         630         640         650
    *   *       *   *       *   *       *   *       *   *
GGACAGTCTG CGGCCCAAGC TGTCTGAGGA GCAGCAGCGC ATCATTGCCA
CCTGTCAGAC GCCGGGTTCG ACAGACTCCT CGTCGTCGCG TAGTAACGGT

      660         670         680         690         700
    *   *       *   *       *   *       *   *       *   *
TACTGCTGGA CGCCCACCAT AAGACCTACG ACCCCACCTA CTCCGACTTC
ATGACGACCT GCGGGTGGTA TTCTGGATGC TGGGGTGGAT GAGGCTGAAG

      710         720         730         740         750
    *   *       *   *       *   *       *   *       *   *
TGCCAGTTCC GGCCTCCAGT TCGTGTGAAT GATGGTGGAG GGAGCCATCC
ACGGTCAAGG CCGGAGGTCA AGCACACTTA CTACCACCTC CCTCGGTAGG

      760         770         780         790         800
    *   *       *   *       *   *       *   *       *   *
TTCCAGGCCC AACTCCAGAC ACACTCCCAG CTTCTCTGGG GACTCCTCCT
AAGGTCCGGG TTGAGGTCTG TGTGAGGGTC GAAGAGACCC CTGAGGAGGA

      810         820         830         840         850
    *   *       *   *       *   *       *   *       *   *
CCTCCTGCTC AGATCACTGT ATCACCTCTT CAGACATGAT GGACTCGTCC
GGAGGACGAG TCTAGTGACA TAGTGGAGAA GTCTGTACTA CCTGAGCAGG

      860         870         880         890         900
    *   *       *   *       *   *       *   *       *   *
AGCTTCTCCA ATCTGGATCT GAGTGAAGAA GATTCAGATG ACCCTTCTGT
TCGAAGAGGT TAGACCTAGA CTCACTTCTT CTAAGTCTAC TGGGAAGACA

      910         920         930         940         950
    *   *       *   *       *   *       *   *       *   *
GACCCTAGAG CTGTCCCAGC TCTCCATGCT GCCCCACCTG GCTGACCTGG
CTGGGATCTC GACAGGGTCG AGAGGTACGA CGGGGTGGAC CGACTGGACC
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FIG. 7C

```
                960       970       980       990      1000
                 *  *      *  *      *  *      *  *      *  *
TCAGTTACAG CATCCAAAAG GTCATTGGCT TTGCTAAGAT GATACCAGGA
AGTCAATGTC GTAGGTTTTC CAGTAACCGA AACGATTCTA CTATGGTCCT

               1010      1020      1030      1040      1050
                 *  *      *  *      *  *      *  *      *  *
TTCAGAGACC TCACCTCTGA GGACCAGATC GTACTGCTGA AGTCAAGTGC
AAGTCTCTGG AGTGGAGACT CCTGGTCTAG CATGACGACT TCAGTTCACG

               1060      1070      1080      1090      1100
                 *  *      *  *      *  *      *  *      *  *
CATTGAGGTC ATCATGTTGC GCTCCAATGA GTCCTTCACC ATGGACGACA
GTAACTCCAG TAGTACAACG CGAGGTTACT CAGGAAGTGG TACCTGCTGT

               1110      1120      1130      1140      1150
                 *  *      *  *      *  *      *  *      *  *
TGTCCTGGAC CTGTGGCAAC CAAGACTACA AGTACCGCGT CAGTGACGTG
ACAGGACCTG GACACCGTTG GTTCTGATGT TCATGGCGCA GTCACTGCAC

               1160      1170      1180      1190      1200
                 *  *      *  *      *  *      *  *      *  *
ACCAAAGCCG GACACAGCCT GGAGCTGATT GAGCCCCTCA TCAAGTTCCA
TGGTTTCGGC CTGTGTCGGA CCTCGACTAA CTCGGGGAGT AGTTCAAGGT

               1210      1220      1230      1240      1250
                 *  *      *  *      *  *      *  *      *  *
GGTGGGACTG AAGAAGCTGA ACTTGCATGA GGAGGAGCAT GTCCTGCTCA
CCACCCTGAC TTCTTCGACT TGAACGTACT CCTCCTCGTA CAGGACGAGT

               1260      1270      1280      1290      1300
                 *  *      *  *      *  *      *  *      *  *
TGGCCATCTG CATCGTCTCC CCAGATCGTC CTGGGGTGCA GGACGCCGCG
ACCGGTAGAC GTAGCAGAGG GGTCTAGCAG GACCCCACGT CCTGCGGCGC

               1310      1320      1330      1340      1350
                 *  *      *  *      *  *      *  *      *  *
CTGATTGAGG CCATCCAGGA CCGCCTGTCC AACACACTGC AGACGTACAT
GACTAACTCC GGTAGGTCCT GGCGGACAGG TTGTGTGACG TCTGCATGTA

               1360      1370      1380      1390      1400
                 *  *      *  *      *  *      *  *      *  *
CCGCTGCCGC CACCCGCCCC CGGGCAGCCA CCTGCTCTAT GCCAAGATGA
GGCGACGGCG GTGGGCGGGG GCCCGTCGGT GGACGAGATA CGGTTCTACT

               1410      1420      1430      1440      1450
                 *  *      *  *      *  *      *  *      *  *
TCCAGAAGCT AGCCGACCTG CGCAGCCTCA ATGAGGAGCA CTCCAAGCAG
AGGTCTTCGA TCGGCTGGAC GCGTCGGAGT TACTCCTCGT GAGGTTCGTC

               1460      1470      1480      1490      1500
                 *  *      *  *      *  *      *  *      *  *
TACCGCTGCC TCTCCTTCCA GCCTGAGTGC AGCATGAAGC TAACGCCCCT
ATGGCGACGG AGAGGAAGGT CGGACTCACG TCGTACTTCG ATTGCGGGGA
```

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FIG. 7D

```
      1510        1520        1530
       *  *        *  *        *  *
TGTGCTCGAA GTGTTTGGCA ATGAGATCTC CTGA (SEQ ID NO:4)
ACACGAGCTT CACAAACCGT TACTCTAGAG GACT (SEQ ID NO:19)
```

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FIG. 8A

```
                                                                  10
                                                                   *
TGCGACCTTG GCGGTGAGCC TGGGGACAGG GGTGAGGCCA GAGACGGACG
ACGCTGGAAC CGCCACTCGG ACCCCTGTCC CCACTCCGGT CTCTGCCTGC

                                                                  60
                                                                   *
GACGCAGGGG CCCGGCCCAA GGCGAGGGAG AACAGCGGCA CTAAGGCAGA
CTGCGTCCCC GGGCCGGGTT CCGCTCCCTC TTGTCGCCGT GATTCCGTCT

                                                                 110
                                                                   *
AAGGAAGAGG GCGGTGTGTT CACCCGCAGC CCAATCCATC ACTCAGCAAC
TTCCTTCTCC CGCCACACAA GTGGGCGTCG GGTTAGGTAG TGAGTCGTTG

                                                                 160
                                                                   *
TCCTAGACGC TGGTAGAAAG TTCCTCCGAG GAGCCTGCCA TCCAGTCGTG
AGGATCTGCG ACCATCTTTC AAGGAGGCTC CTCGGACGGT AGGTCAGCAC

                                                                 210
                                                                   *
CGTGCAGAAG CCTTTGGGTC TGAAGTGTCT GTGAGACCTC ACAGAAGAGC
GCACGTCTTC GGAAACCCAG ACTTCACAGA CACTCTGGAG TGTCTTCTCG

                                                                 260
                                                                   *
ACCCCTGGGC TCCACTTACC TGCCCCCTGC TCCTTCAGGG ATGGAGGCAA
TGGGGACCCG AGGTGAATGG ACGGGGGACG AGGAAGTCCC TACCTCCGTT
                                                       MetGluAla>

                                                                 310
                                                                   *
TGGCGGCCAG CACTTCCCTG CCTGACCCTG GAGACTTTGA CCGGAACGTG
ACCGCCGGTC GTGAAGGGAC GGACTGGGAC CTCTGAAACT GGCCTTGCAC
MetAlaAlaSer ThrSerLeu ProAspPro GlyAspPheAsp ArgAsnVal>

                                                                 360
                                                                   *
CCCCGGATCT GTGGGGTGTG TGGAGACCGA GCCACTGGCT TTCACTTCAA
GGGGCCTAGA CACCCCACAC ACCTCTGGCT CGGTGACCGA AAGTGAAGTT
ProArgIle CysGlyValCys GlyAspArg AlaThrGly PheHisPheAsn>

                                                                 410
                                                                   *
TGCTATGACC TGTGAAGGCT GCAAAGGCTT CTTCAGGCGA AGCATGAAGC
ACGATACTGG ACACTTCCGA CGTTTCCGAA GAAGTCCGCT TCGTACTTCG
 AlaMetThr CysGluGly CysLysGlyPhe PheArgArg SerMetLys>

                                                                 460
                                                                   *
GGAAGGCACT ATTCACCTGC CCCTTCAACG GGGACTGCCG CATCACCAAG
CCTTCCGTGA TAAGTGGACG GGGAAGTTGC CCCTGACGGC GTAGTGGTTC
ArgLysAlaLeu PheThrCys ProPheAsn GlyAspCysArg IleThrLys>
```

Title: "Isoforms of the Human Vitamin D Receptor"
Inventor: Linda Anne Crofts
Application No.: 09/509,482
Atty. Docket No. RICE-014

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FIG. 8B

```
          510         520         530         540         550
           *           *           *           *           *
GACAACCGAC GCCACTGCCA GGCCTGCCGG CTCAAACGCT GTGTGGACAT
CTGTTGGCTG CGGTGACGGT CCGGACGGCC GAGTTTGCGA CACACCTGTA
AspAsnArg ArgHisCysGln AlaCysArg LeuLysArg CysValAspIle>

          560         570         580         590         600
           *           *           *           *           *
CGGCATGATG AAGGAGTTCA TTCTGACAGA TGAGGAAGTG CAGAGGAAGC
GCCGTACTAC TTCCTCAAGT AAGACTGTCT ACTCCTTCAC GTCTCCTTCG
 GlyMetMet LysGluPhe IleLeuThrAsp GluGluVal GlnArgLys>

          610         620         630         640         650
           *           *           *           *           *
GGGAGATGAT CCTGAAGCGG AAGGAGGAGG AGGCCTTGAA GGACAGTCTG
CCCTCTACTA GGACTTCGCC TTCCTCCTCC TCCGGAACTT CCTGTCAGAC
ArgGluMetIle LeuLysArg LysGluGlu GluAlaLeuLys AspSerLeu>

          660         670         680         690         700
           *           *           *           *           *
CGGCCCAAGC TGTCTGAGGA GCAGCAGCGC ATCATTGCCA TACTGCTGGA
GCCGGGTTCG ACAGACTCCT CGTCGTCGCG TAGTAACGGT ATGACGACCT
ArgProLys LeuSerGluGlu GlnGlnArg IleIleAla IleLeuLeuAsp>

          710         720         730         740         750
           *           *           *           *           *
CGCCCACCAT AAGACCTACG ACCCCACCTA CTCCGACTTC TGCCAGTTCC
GCGGGTGGTA TTCTGGATGC TGGGGTGGAT GAGGCTGAAG ACGGTCAAGG
 AlaHisHis LysThrTyr AspProThrTyr SerAspPhe CysGlnPhe>

          760         770         780         790         800
           *           *           *           *           *
GGCCTCCAGT TCGTGTGAAT GATGGTGGAG GGAGCCATCC TTCCAGGCCC
CCGGAGGTCA AGCACACTTA CTACCACCTC CCTCGGTAGG AAGGTCCGGG
ArgProProVal ArgValAsn AspGlyGly GlySerHisPro SerArgPro>

          810         820         830         840         850
           *           *           *           *           *
AACTCCAGAC ACACTCCCAG CTTCTCTGGG GACTCCTCCT CCTCCTGCTC
TTGAGGTCTG TGTGAGGGTC GAAGAGACCC CTGAGGAGGA GGAGGACGAG
AsnSerArg HisThrProSer PheSerGly AspSerSer SerSerCysSer>

          860         870         880         890         900
           *           *           *           *           *
AGATCACTGT ATCACCTCTT CAGACATGAT GGACTCGTCC AGCTTCTCCA
TCTAGTGACA TAGTGGAGAA GTCTGTACTA CCTGAGCAGG TCGAAGAGGT
 AspHisCys IleThrSer SerAspMetMet AspSerSer SerPheSer>

          910         920         930         940         950
           *           *           *           *           *
ATCTGGATCT GAGTGAAGAA GATTCAGATG ACCCTTCTGT GACCCTAGAG
TAGACCTAGA CTCACTTCTT CTAAGTCTAC TGGGAAGACA CTGGGATCTC
AsnLeuAspLeu SerGluGlu AspSerAsp AspProSerVal ThrLeuGlu>

          960         970         980         990        1000
           *           *           *           *           *
CTGTCCCAGC TCTCCATGCT GCCCCACCTG GCTGACCTGG TCAGTTACAG
GACAGGGTCG AGAGGTACGA CGGGGTGGAC CGACTGGACC AGTCAATGTC
LeuSerGln LeuSerMetLeu ProHisLeu AlaAspLeu ValSerTyrSer>
```

Title: "Isoforms of the Human Vitamin D Receptor"
Inventor: Linda Anne Crofts
Application No.: 09/509,482
Atty. Docket No. RICE-014

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FIG. 8C

```
                1010        1020        1030        1040        1050
                  *           *           *           *           *
CATCCAAAAG GTCATTGGCT TTGCTAAGAT GATACCAGGA TTCAGAGACC
GTAGGTTTTC CAGTAACCGA AACGATTCTA CTATGGTCCT AAGTCTCTGG
 IleGlnLys ValIleGly PheAlaLysMet IleProGly PheArgAsp>

                1060        1070        1080        1090        1100
                  *           *           *           *           *
TCACCTCTGA GGACCAGATC GTACTGCTGA AGTCAAGTGC CATTGAGGTC
AGTGGAGACT CCTGGTCTAG CATGACGACT TCAGTTCACG GTAACTCCAG
LeuThrSerGlu AspGlnIle ValLeuLeu LysSerSerAla IleGluVal>

                1110        1120        1130        1140        1150
                  *           *           *           *           *
ATCATGTTGC GCTCCAATGA GTCCTTCACC ATGGACGACA TGTCCTGGAC
TAGTACAACG CGAGGTTACT CAGGAAGTGG TACCTGCTGT ACAGGACCTG
 IleMetLeu ArgSerAsnGlu SerPheThr MetAspAsp MetSerTrpThr>

                1160        1170        1180        1190        1200
                  *           *           *           *           *
CTGTGGCAAC CAAGACTACA AGTACCGCGT CAGTGACGTG ACCAAAGCCG
GACACCGTTG GTTCTGATGT TCATGGCGCA GTCACTGCAC TGGTTTCGGC
 CysGlyAsn GlnAspTyr LysTyrArgVal SerAspVal ThrLysAla>

                1210        1220        1230        1240        1250
                  *           *           *           *           *
GACACAGCCT GGAGCTGATT GAGCCCCTCA TCAAGTTCCA GGTGGGACTG
CTGTGTCGGA CCTCGACTAA CTCGGGGAGT AGTTCAAGGT CCACCCTGAC
GlyHisSerLeu GluLeuIle GluProLeu IleLysPheGln ValGlyLeu>

                1260        1270        1280        1290        1300
                  *           *           *           *           *
AAGAAGCTGA ACTTGCATGA GGAGGAGCAT GTCCTGCTCA TGGCCATCTG
TTCTTCGACT TGAACGTACT CCTCCTCGTA CAGGACGAGT ACCGGTAGAC
 LysLysLeu AsnLeuHisGlu GluGluHis ValLeuLeu MetAlaIleCys>

                1310        1320        1330        1340        1350
                  *           *           *           *           *
CATCGTCTCC CCAGATCGTC CTGGGGTGCA GGACGCCGCG CTGATTGAGG
GTAGCAGAGG GGTCTAGCAG GACCCCACGT CCTGCGGCGC GACTAACTCC
 IleValSer ProAspArg ProGlyValGln AspAlaAla LeuIleGlu>

                1360        1370        1380        1390        1400
                  *           *           *           *           *
CCATCCAGGA CCGCCTGTCC AACACACTGC AGACGTACAT CCGCTGCCGC
GGTAGGTCCT GGCGGACAGG TTGTGTGACG TCTGCATGTA GGCGACGGCG
AlaIleGlnAsp ArgLeuSer AsnThrLeu GlnThrTyrIle ArgCysArg>

                1410        1420        1430        1440        1450
                  *           *           *           *           *
CACCCGCCCC CGGGCAGCCA CCTGCTCTAT GCCAAGATGA TCCAGAAGCT
GTGGGCGGGG GCCCGTCGGT GGACGAGATA CGGTTCTACT AGGTCTTCGA
HisProPro ProGlySerHis LeuLeuTyr AlaLysMet IleGlnLysLeu>

                1460        1470        1480        1490        1500
                  *           *           *           *           *
AGCCGACCTG CGCAGCCTCA ATGAGGAGCA CTCCAAGCAG TACCGCTGCC
TCGGCTGGAC GCGTCGGAGT TACTCCTCGT GAGGTTCGTC ATGGCGACGG
 AlaAspLeu ArgSerLeu AsnGluGluHis SerLysGln TyrArgCys>
```

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FIG. 8D

```
      1510        1520        1530        1540        1550
         *           *           *           *           *
TCTCCTTCCA GCCTGAGTGC AGCATGAAGC TAACGCCCCT TGTGCTCGAA
AGAGGAAGGT CGGACTCACG TCGTACTTCG ATTGCGGGGA ACACGAGCTT
LeuSerPheGln ProGluCys SerMetLys LeuThrProLeu ValLeuGlu>

      1560        1570
         *           *
GTGTTTGGCA ATGAGATCTC CTGA (SEQ ID NO:7)
CACAAACCGT TACTCTAGAG GACT (SEQ ID NO:20)
ValPheGly AsnGluIleSer ***> (SEQ ID NO:12)
```

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Title: "Isoforms of the Human Vitamin D Receptor"
Inventor: Linda Anne Crofts
Application No.: 09/509,482
Atty. Docket No. RICE-014

Fig. 1A.

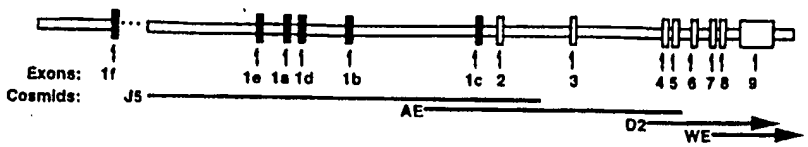


Fig. 1B.

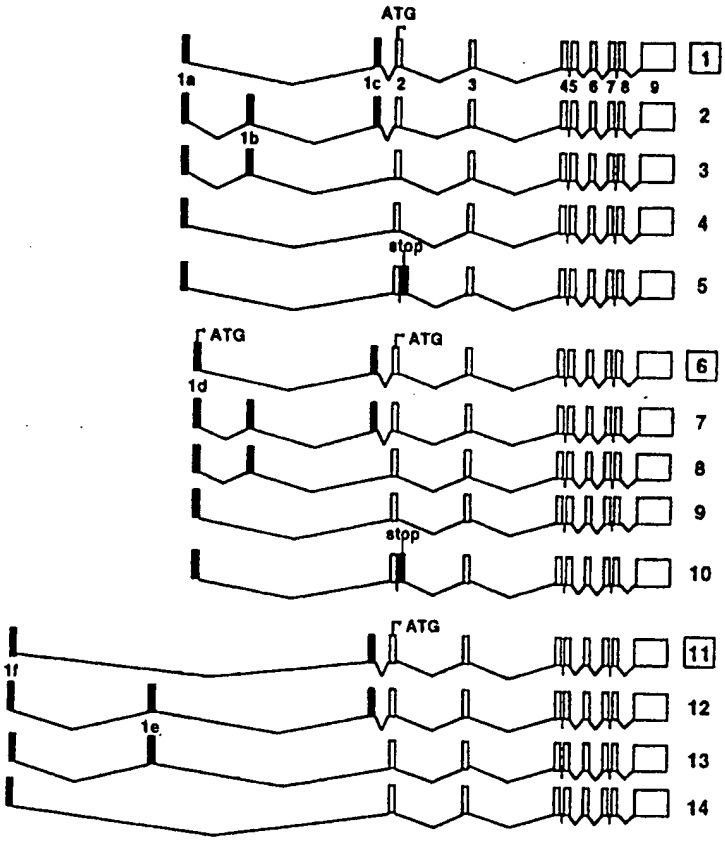
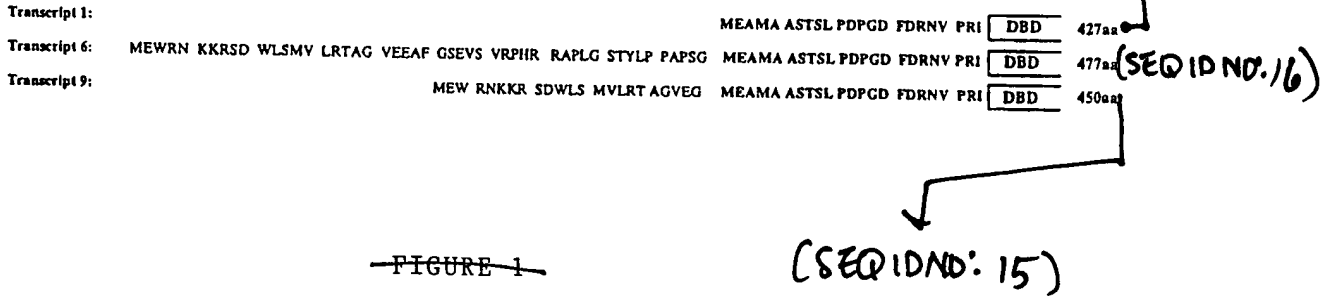


Fig. 1C.



~~FIGURE 1~~

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A. 5'...atcccttaag GGCTCCTGAACCTAGCCCAGCTGGACGGAG
AAATGGACTCTAGCCTCCTCTGATAGCCTCATGCCAGGCCC
CGTGCACATTGCTTTGCTTGCCTCCCTCAATCCTCATAGCT
TCTCTTTGGGgtaagtacag...3' (SEQ ID NO: 13)

B. 5'...TGCGACCTTGGCGGTGAGCCTGGGGACAGGGGTGAGGC
CAGAGACGGACGGACGCAGGGGCCCGGCCCAAGGCGAGGG
AGAACAGCGGCACTAAGGCAGAAAGGAAGAGGGCGGTGTG
TTCACCCGCAGCCCAATCCATCACTCAGCAACTCCTAGAC
GCTGGTAGAAAGTTCCTCCGAGGAGCCTGCCATCCAGTCGT
GCGTGCAG...3' (SEQ ID NO: 5)

C. 5'...tgtttttag AGGCAGCATGAAACAGTGGGATGTGCAGAG
AGAAGATCTGGGTCCAGTAGCTCTGACACTCCTCAGCTGT
AGAAACCTTGACAACTCTGCACATCAGTTGTACAATGGAA
CGGTATTTTTTACTCTTCATGTCTGAAAAGGCTATGATAA
AGATCAAgtaagatatt...3' (SEQ ID NO: 6)

D. 5'...GTTTCCTTCTTCTGTCGGGGCGCCTTGGCATGGAGTGG
AGGAATAAGAAAAGGAGCGATTGGCTGTCGATGGTGCTCA
GAACTGCTGGAGTGGAGGgtgtgtaacc...3' (SEQ ID NO: 1)

FIG. 4
~~FIGURE 4~~

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FIG. 5A
~~FIGURE 5A~~

TRANSCRIPT 6

(Sequence Range: 1 to 1463)

```
                10        20        30        40        50
        *   *   *   *   *   *   *   *   *   *   *   *   *
GTTTCCTTCT TCTGTCGGGG CGCCTTGGCA TGGAGTGGAG GAATAAGAAA
CAAAGGAAGA AGACAGCCCC GCGGAACCGT ACCTCACCTC CTTATTCTTT
                                  MetGluTrpArg AsnLysLys>

                60        70        80        90        100
        *   *   *   *   *   *   *   *   *   *   *   *   *
AGGAGCGATT GGCTGTCGAT GGTGCTCAGA ACTGCTGGAG TGGAGGAAGC
TCCTCGCTAA CCGACAGCTA CCACGAGTCT TGACGACCTC ACCTCCTTCG
ArgSerAsp TrpLeuSerMet ValLeuArg ThrAlaGly ValGluGluAla>

                110       120       130       140       150
        *   *   *   *   *   *   *   *   *   *   *   *   *
CTTTGGGTCT GAAGTGTCTG TGAGACCTCA CAGAAGAGCA CCCCTGGGCT
GAAACCCAGA CTTCACAGAC ACTCTGGAGT GTCTTCTCGT GGGGACCCGA
 PheGlySer GluValSer ValArgProHis ArgArgAla ProLeuGly>

                160       170       180       190       200
        *   *   *   *   *   *   *   *   *   *   *   *   *
CCACTTACCT GCCCCCTGCT CCTTCAGGGA TGGAGGCAAT GGCGGCCAGC
GGTGAATGGA CGGGGGACGA GGAAGTCCCT ACCTCCGTTA CCGCCGGTCG
SerThrTyrLeu ProProAla ProSerGly MetGluAlaMet AlaAlaSer>

                210       220       230       240       250
        *   *   *   *   *   *   *   *   *   *   *   *   *
ACTTCCCTGC CTGACCCTGG AGACTTTGAC CGGAACGTGC CCCGGATCTG
TGAAGGGACG GACTGGGACC TCTGAAACTG GCCTTGCACG GGGCCTAGAC
ThrSerLeu ProAspProGly AspPheAsp ArgAsnVal ProArgIleCys>

                260       270       280       290       300
        *   *   *   *   *   *   *   *   *   *   *   *   *
TGGGGTGTGT GGAGACCGAG CCACTGGCTT TCACTTCAAT GCTATGACCT
ACCCCACACA CCTCTGGCTC GGTGACCGAA AGTGAAGTTA CGATACTGGA
 GlyValCys GlyAspArg AlaThrGlyPhe HisPheAsn AlaMetThr>

                310       320       330       340       350
        *   *   *   *   *   *   *   *   *   *   *   *   *
GTGAAGGCTG CAAAGGCTTC TTCAGGCGAA GCATGAAGCG GAAGGCACTA
CACTTCCGAC GTTTCCGAAG AAGTCCGCTT CGTACTTCGC CTTCCGTGAT
CysGluGlyCys LysGlyPhe PheArgArg SerMetLysArg LysAlaLeu>

                360       370       380       390       400
        *   *   *   *   *   *   *   *   *   *   *   *   *
TTCACCTGCC CCTTCAACGG GGACTGCCGC ATCACCAAGG ACAACCGACG
AAGTGGACGG GGAAGTTGCC CCTGACGGCG TAGTGGTTCC TGTTGGCTGC
PheThrCys ProPheAsnGly AspCysArg IleThrLys AspAsnArgArg>
```

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FIGURE 5B


```
        410         420         430         440         450
    *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
CCACTGCCAG GCCTGCCGGC TCAAACGCTG TGTGGACATC GGCATGATGA
GGTGACGGTC CGGACGGCCG AGTTTGCGAC ACACCTGTAG CCGTACTACT
 HisCysGln AlaCysArg LeuLysArgCys ValAspIle GlyMetMet>

        460         470         480         490         500
    *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
AGGAGTTCAT TCTGACAGAT GAGGAAGTGC AGAGGAAGCG GGAGATGATC
TCCTCAAGTA AGACTGTCTA CTCCTTCACG TCTCCTTCGC CCTCTACTAG
LysGluPheIle LeuThrAsp GluGluVal GlnArgLysArg GluMetIle>

        510         520         530         540         550
    *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
CTGAAGCGGA AGGAGGAGGA GGCCTTGAAG GACAGTCTGC GGCCCAAGCT
GACTTCGCCT TCCTCCTCCT CCGGAACTTC CTGTCAGACG CCGGGTTCGA
LeuLysArg LysGluGluGlu AlaLeuLys AspSerLeu ArgProLysLeu>

        560         570         580         590         600
    *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
GTCTGAGGAG CAGCAGCGCA TCATTGCCAT ACTGCTGGAC GCCCACCATA
CAGACTCCTC GTCGTCGCGT AGTAACGGTA TGACGACCTG CGGGTGGTAT
 SerGluGlu GlnGlnArg IleIleAlaIle LeuLeuAsp AlaHisHis>

        610         620         630         640         650
    *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
AGACCTACGA CCCCACCTAC TCCGACTTCT GCCAGTTCCG GCCTCCAGTT
TCTGGATGCT GGGGTGGATG AGGCTGAAGA CGGTCAAGGC CGGAGGTCAA
LysThrTyrAsp ProThrTyr SerAspPhe CysGlnPheArg ProProVal>

        660         670         680         690         700
    *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
CGTGTGAATG ATGGTGGAGG GAGCCATCCT TCCAGGCCCA ACTCCAGACA
GCACACTTAC TACCACCTCC CTCGGTAGGA AGGTCCGGGT TGAGGTCTGT
ArgValAsn AspGlyGlyGly SerHisPro SerArgPro AsnSerArgHis>

        710         720         730         740         750
    *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
CACTCCCAGC TTCTCTGGGG ACTCCTCCTC CTCCTGCTCA GATCACTGTA
GTGAGGGTCG AAGAGACCCC TGAGGAGGAG GAGGACGAGT CTAGTGACAT
 ThrProSer PheSerGly AspSerSerSer SerCysSer AspHisCys>

        760         770         780         790         800
    *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
TCACCTCTTC AGACATGATG GACTCGTCCA GCTTCTCCAA TCTGGATCTG
AGTGGAGAAG TCTGTACTAC CTGAGCAGGT CGAAGAGGTT AGACCTAGAC
IleThrSerSer AspMetMet AspSerSer SerPheSerAsn LeuAspLeu>

        810         820         830         840         850
    *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
AGTGAAGAAG ATTCAGATGA CCCTTCTGTG ACCCTAGAGC TGTCCCAGCT
TCACTTCTTC TAAGTCTACT GGGAAGACAC TGGGATCTCG ACAGGGTCGA
SerGluGlu AspSerAspAsp ProSerVal ThrLeuGlu LeuSerGlnLeu>
```

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FIG. 7A

~~FIGURE 7~~

TRANSCRIPT 10

(Sequence Range: 1 to 1534)

```
                                                                    50
                10        20        30        40        *         *
        *       *   *     *   *     *   *     *   *     *         *
GTTTCCTTCT TCTGTCGGGG CGCCTTGGCA TGGAGTGGAG GAATAAGAAA
CAAAGGAAGA AGACAGCCCC GCGGAACCGT ACCTCACCTC CTTATTCTTT
                                  MetGluTrpArg AsnLysLys>

                                                                   100
                60        70        80        90        *         *
        *       *   *     *   *     *   *     *   *     *         *
AGGAGCGATT GGCTGTCGAT GGTGCTCAGA ACTGCTGGAG TGGAGGGGAT
TCCTCGCTAA CCGACAGCTA CCACGAGTCT TGACGACCTC ACCTCCCCTA
ArgSerAsp TrpLeuSerMet ValLeuArg ThrAlaGly ValGluGlyMet>

                                                                   150
               110       120       130       140       *         *
        *      *   *     *   *     *   *     *   *     *         *
GGAGGCAATG GCGGCCAGCA CTTCCCTGCC TGACCCTGGA GACTTTGACC
CCTCCGTTAC CGCCGGTCGT GAAGGGACGG ACTGGGACCT CTGAAACTGG
 GluAlaMet AlaAlaSer ThrSerLeuPro AspProGly AspPheAsp>

                                                                   200
               160       170       180       190       *         *
        *      *   *     *   *     *   *     *   *     *         *
GGAACGTGCC CCGGATCTGT GGGGTGTGTG GAGACCGAGC CACTGGCTTT
CCTTGCACGG GGCCTAGACA CCCCACACAC CTCTGGCTCG GTGACCGAAA
ArgAsnValPro ArgIleCys GlyValCys GlyAspArgAla ThrGlyPhe>

                                                                   250
               210       220       230       240       *         *
        *      *   *     *   *     *   *     *   *     *         *
CACTTCAATG CTATGACCTG TGAAGGCTGC AAAGGCTTCT TCAGGTGAGC
GTGAAGTTAC GATACTGGAC ACTTCCGACG TTTCCGAAGA AGTCCACTCG
HisPheAsn AlaMetThrCys GluGlyCys LysGlyPhe PheArg***

                                                                   300
               260       270       280       290       *         *
        *      *   *     *   *     *   *     *   *     *         *
CCCCCTCCCA GGCTCTCCCC AGTGGAAAGG GAGGGAGAAG AAGCAAGGTG
GGGGGAGGGT CCGAGAGGGG TCACCTTTCC CTCCCTCTTC TTCGTTCCAC

                                                                   350
               310       320       330       340       *         *
        *      *   *     *   *     *   *     *   *     *         *
TTTCCATGAA GGGAGCCCTT GCATTTTTCA CATCTCCTTC CTTACAATGT
AAAGGTACTT CCCTCGGGAA CGTAAAAAGT GTAGAGGAAG GAATGTTACA

                                                                   400
               360       370       380       390       *         *
        *      *   *     *   *     *   *     *   *     *         *
CCATGGAACA TGCGGCGCTC ACAGCCACAG GAGCAGGAGG GTCTTGGCGA
GGTACCTTGT ACGCCGCGAG TGTCGGTGTC CTCGTCCTCC CAGAACCGCT
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FIG. 7B


```
       410         420         430         440         450
    *   *   *   *   *   *   *   *   *   *
AGCATGAAGC GGAAGGCACT ATTCACCTGC CCCTTCAACG GGGACTGCCG
TCGTACTTCG CCTTCCGTGA TAAGTGGACG GGGAAGTTGC CCCTGACGGC

       460         470         480         490         500
    *   *   *   *   *   *   *   *   *   *
CATCACCAAG GACAACCGAC GCCACTGCCA GGCCTGCCGG CTCAAACGCT
GTAGTGGTTC CTGTTGGCTG CGGTGACGGT CCGGACGGCC GAGTTTGCGA

       510         520         530         540         550
    *   *   *   *   *   *   *   *   *   *
GTGTGGACAT CGGCATGATG AAGGAGTTCA TTCTGACAGA TGAGGAAGTG
CACACCTGTA GCCGTACTAC TTCCTCAAGT AAGACTGTCT ACTCCTTCAC

       560         570         580         590         600
    *   *   *   *   *   *   *   *   *   *
CAGAGGAAGC GGGAGATGAT CCTGAAGCGG AAGGAGGAGG AGGCCTTGAA
GTCTCCTTCG CCCTCTACTA GGACTTCGCC TTCCTCCTCC TCCGGAACTT

       610         620         630         640         650
    *   *   *   *   *   *   *   *   *   *
GGACAGTCTG CGGCCCAAGC TGTCTGAGGA GCAGCAGCGC ATCATTGCCA
CCTGTCAGAC GCCGGGTTCG ACAGACTCCT CGTCGTCGCG TAGTAACGGT

       660         670         680         690         700
    *   *   *   *   *   *   *   *   *   *
TACTGCTGGA CGCCCACCAT AAGACCTACG ACCCCACCTA CTCCGACTTC
ATGACGACCT GCGGGTGGTA TTCTGGATGC TGGGGTGGAT GAGGCTGAAG

       710         720         730         740         750
    *   *   *   *   *   *   *   *   *   *
TGCCAGTTCC GGCCTCCAGT TCGTGTGAAT GATGGTGGAG GGAGCCATCC
ACGGTCAAGG CCGGAGGTCA AGCACACTTA CTACCACCTC CCTCGGTAGG

       760         770         780         790         800
    *   *   *   *   *   *   *   *   *   *
TTCCAGGCCC AACTCCAGAC ACACTCCCAG CTTCTCTGGG GACTCCTCCT
AAGGTCCGGG TTGAGGTCTG TGTGAGGGTC GAAGAGACCC CTGAGGAGGA

       810         820         830         840         850
    *   *   *   *   *   *   *   *   *   *
CCTCCTGCTC AGATCACTGT ATCACCTCTT CAGACATGAT GGACTCGTCC
GGAGGACGAG TCTAGTGACA TAGTGGAGAA GTCTGTACTA CCTGAGCAGG

       860         870         880         890         900
    *   *   *   *   *   *   *   *   *   *
AGCTTCTCCA ATCTGGATCT GAGTGAAGAA GATTCAGATG ACCCTTCTGT
TCGAAGAGGT TAGACCTAGA CTCACTTCTT CTAAGTCTAC TGGGAAGACA

       910         920         930         940         950
    *   *   *   *   *   *   *   *   *   *
GACCCTAGAG CTGTCCCAGC TCTCCATGCT GCCCCACCTG GCTGACCTGG
CTGGGATCTC GACAGGGTCG AGAGGTACGA CGGGGTGGAC CGACTGGACC
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FIG. 7C


```
                960       970       980       990      1000
                 *  *      *  *      *  *      *  *      *  *
TCAGTTACAG CATCCAAAAG GTCATTGGCT TTGCTAAGAT GATACCAGGA
AGTCAATGTC GTAGGTTTTC CAGTAACCGA AACGATTCTA CTATGGTCCT

               1010      1020      1030      1040      1050
                 *  *      *  *      *  *      *  *      *  *
TTCAGAGACC TCACCTCTGA GGACCAGATC GTACTGCTGA AGTCAAGTGC
AAGTCTCTGG AGTGGAGACT CCTGGTCTAG CATGACGACT TCAGTTCACG

               1060      1070      1080      1090      1100
                 *  *      *  *      *  *      *  *      *  *
CATTGAGGTC ATCATGTTGC GCTCCAATGA GTCCTTCACC ATGGACGACA
GTAACTCCAG TAGTACAACG CGAGGTTACT CAGGAAGTGG TACCTGCTGT

               1110      1120      1130      1140      1150
                 *  *      *  *      *  *      *  *      *  *
TGTCCTGGAC CTGTGGCAAC CAAGACTACA AGTACCGCGT CAGTGACGTG
ACAGGACCTG GACACCGTTG GTTCTGATGT TCATGGCGCA GTCACTGCAC

               1160      1170      1180      1190      1200
                 *  *      *  *      *  *      *  *      *  *
ACCAAAGCCG GACACAGCCT GGAGCTGATT GAGCCCCTCA TCAAGTTCCA
TGGTTTCGGC CTGTGTCGGA CCTCGACTAA CTCGGGGAGT AGTTCAAGGT

               1210      1220      1230      1240      1250
                 *  *      *  *      *  *      *  *      *  *
GGTGGGACTG AAGAAGCTGA ACTTGCATGA GGAGGAGCAT GTCCTGCTCA
CCACCCTGAC TTCTTCGACT TGAACGTACT CCTCCTCGTA CAGGACGAGT

               1260      1270      1280      1290      1300
                 *  *      *  *      *  *      *  *      *  *
TGGCCATCTG CATCGTCTCC CCAGATCGTC CTGGGGTGCA GGACGCCGCG
ACCGGTAGAC GTAGCAGAGG GGTCTAGCAG GACCCCACGT CCTGCGGCGC

               1310      1320      1330      1340      1350
                 *  *      *  *      *  *      *  *      *  *
CTGATTGAGG CCATCCAGGA CCGCCTGTCC AACACACTGC AGACGTACAT
GACTAACTCC GGTAGGTCCT GGCGGACAGG TTGTGTGACG TCTGCATGTA

               1360      1370      1380      1390      1400
                 *  *      *  *      *  *      *  *      *  *
CCGCTGCCGC CACCCGCCCC CGGGCAGCCA CCTGCTCTAT GCCAAGATGA
GGCGACGGCG GTGGGCGGGG GCCCGTCGGT GGACGAGATA CGGTTCTACT

               1410      1420      1430      1440      1450
                 *  *      *  *      *  *      *  *      *  *
TCCAGAAGCT AGCCGACCTG CGCAGCCTCA ATGAGGAGCA CTCCAAGCAG
AGGTCTTCGA TCGGCTGGAC GCGTCGGAGT TACTCCTCGT GAGGTTCGTC

               1460      1470      1480      1490      1500
                 *  *      *  *      *  *      *  *      *  *
TACCGCTGCC TCTCCTTCCA GCCTGAGTGC AGCATGAAGC TAACGCCCCT
ATGGCGACGG AGAGGAAGGT CGGACTCACG TCGTACTTCG ATTGCGGGGA
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FIG. 7D


```
     1510        1520        1530
      *   *       *   *       *   *
TGTGCTCGAA GTGTTTGGCA ATGAGATCTC CTGA   (SEQ ID NO:4)
ACACGAGCTT CACAAACCGT TACTCTAGAG GACT   (SEQ ID NO:19)
```

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FIG. 8A

~~FIGURE 8~~

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```
                                                                    10         20         30         40         50
                                                                     *          *          *          *          *
TGCGACCTTG GCGGTGAGCC TGGGGACAGG GGTGAGGCCA GAGACGGACG
ACGCTGGAAC CGCCACTCGG ACCCCTGTCC CCACTCCGGT CTCTGCCTGC

        60         70         80         90        100
         *          *          *          *          *
GACGCAGGGG CCCGGCCCAA GGCGAGGGAG AACAGCGGCA CTAAGGCAGA
CTGCGTCCCC GGGCCGGGTT CCGCTCCCTC TTGTCGCCGT GATTCCGTCT

       110        120        130        140        150
         *          *          *          *          *
AAGGAAGAGG GCGGTGTGTT CACCCGCAGC CCAATCCATC ACTCAGCAAC
TTCCTTCTCC CGCCACACAA GTGGGCGTCG GGTTAGGTAG TGAGTCGTTG

       160        170        180        190        200
         *          *          *          *          *
TCCTAGACGC TGGTAGAAAG TTCCTCCGAG GAGCCTGCCA TCCAGTCGTG
AGGATCTGCG ACCATCTTTC AAGGAGGCTC CTCGGACGGT AGGTCAGCAC

       210        220        230        240        250
         *          *          *          *          *
CGTGCAGAAG CCTTTGGGTC TGAAGTGTCT GTGAGACCTC ACAGAAGAGC
GCACGTCTTC GGAAACCCAG ACTTCACAGA CACTCTGGAG TGTCTTCTCG

       260        270        280        290        300
         *          *          *          *          *
ACCCCTGGGC TCCACTTACC TGCCCCCTGC TCCTTCAGGG ATGGAGGCAA
TGGGGACCCG AGGTGAATGG ACGGGGGACG AGGAAGTCCC TACCTCCGTT
                                                  MetGluAla>

       310        320        330        340        350
         *          *          *          *          *
TGGCGGCCAG CACTTCCCTG CCTGACCCTG GAGACTTTGA CCGGAACGTG
ACCGCCGGTC GTGAAGGGAC GGACTGGGAC CTCTGAAACT GGCCTTGCAC
MetAlaAlaSer ThrSerLeu ProAspPro GlyAspPheAsp ArgAsnVal>

       360        370        380        390        400
         *          *          *          *          *
CCCCGGATCT GTGGGGTGTG TGGAGACCGA GCCACTGGCT TTCACTTCAA
GGGGCCTAGA CACCCCACAC ACCTCTGGCT CGGTGACCGA AAGTGAAGTT
ProArgIle CysGlyValCys GlyAspArg AlaThrGly PheHisPheAsn>

       410        420        430        440        450
         *          *          *          *          *
TGCTATGACC TGTGAAGGCT GCAAAGGCTT CTTCAGGCGA AGCATGAAGC
ACGATACTGG ACACTTCCGA CGTTTCCGAA GAAGTCCGCT TCGTACTTCG
 AlaMetThr CysGluGly CysLysGlyPhe PheArgArg SerMetLys>

       460        470        480        490        500
         *          *          *          *          *
GGAAGGCACT ATTCACCTGC CCCTTCAACG GGGACTGCCG CATCACCAAG
CCTTCCGTGA TAAGTGGACG GGGAAGTTGC CCCTGACGGC GTAGTGGTTC
ArgLysAlaLeu PheThrCys ProPheAsn GlyAspCysArg IleThrLys>
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FIG. 8B


```
        510         520         530         540         550
          *           *           *           *           *
 GACAACCGAC GCCACTGCCA GGCCTGCCGG CTCAAACGCT GTGTGGACAT
 CTGTTGGCTG CGGTGACGGT CCGGACGGCC GAGTTTGCGA CACACCTGTA
 AspAsnArg ArgHisCysGln AlaCysArg LeuLysArg CysValAspIle>

        560         570         580         590         600
          *           *           *           *           *
 CGGCATGATG AAGGAGTTCA TTCTGACAGA TGAGGAAGTG CAGAGGAAGC
 GCCGTACTAC TTCCTCAAGT AAGACTGTCT ACTCCTTCAC GTCTCCTTCG
  GlyMetMet LysGluPhe IleLeuThrAsp GluGluVal GlnArgLys>

        610         620         630         640         650
          *           *           *           *           *
 GGGAGATGAT CCTGAAGCGG AAGGAGGAGG AGGCCTTGAA GGACAGTCTG
 CCCTCTACTA GGACTTCGCC TTCCTCCTCC TCCGGAACTT CCTGTCAGAC
ArgGluMetIle LeuLysArg LysGluGlu GluAlaLeuLys AspSerLeu>

        660         670         680         690         700
          *           *           *           *           *
 CGGCCCAAGC TGTCTGAGGA GCAGCAGCGC ATCATTGCCA TACTGCTGGA
 GCCGGGTTCG ACAGACTCCT CGTCGTCGCG TAGTAACGGT ATGACGACCT
 ArgProLys LeuSerGluGlu GlnGlnArg IleIleAla IleLeuLeuAsp>

        710         720         730         740         750
          *           *           *           *           *
 CGCCCACCAT AAGACCTACG ACCCCACCTA CTCCGACTTC TGCCAGTTCC
 GCGGGTGGTA TTCTGGATGC TGGGGTGGAT GAGGCTGAAG ACGGTCAAGG
  AlaHisHis LysThrTyr AspProThrTyr SerAspPhe CysGlnPhe>

        760         770         780         790         800
          *           *           *           *           *
 GGCCTCCAGT TCGTGTGAAT GATGGTGGAG GGAGCCATCC TTCCAGGCCC
 CCGGAGGTCA AGCACACTTA CTACCACCTC CCTCGGTAGG AAGGTCCGGG
ArgProProVal ArgValAsn AspGlyGly GlySerHisPro SerArgPro>

        810         820         830         840         850
          *           *           *           *           *
 AACTCCAGAC ACACTCCCAG CTTCTCTGGG GACTCCTCCT CCTCCTGCTC
 TTGAGGTCTG TGTGAGGGTC GAAGAGACCC CTGAGGAGGA GGAGGACGAG
 AsnSerArg HisThrProSer PheSerGly AspSerSer SerSerCysSer>

        860         870         880         890         900
          *           *           *           *           *
 AGATCACTGT ATCACCTCTT CAGACATGAT GGACTCGTCC AGCTTCTCCA
 TCTAGTGACA TAGTGGAGAA GTCTGTACTA CCTGAGCAGG TCGAAGAGGT
  AspHisCys IleThrSer SerAspMetMet AspSerSer SerPheSer>

        910         920         930         940         950
          *           *           *           *           *
 ATCTGGATCT GAGTGAAGAA GATTCAGATG ACCCTTCTGT GACCCTAGAG
 TAGACCTAGA CTCACTTCTT CTAAGTCTAC TGGGAAGACA CTGGGATCTC
AsnLeuAspLeu SerGluGlu AspSerAsp AspProSerVal ThrLeuGlu>

        960         970         980         990        1000
          *           *           *           *           *
 CTGTCCCAGC TCTCCATGCT GCCCCACCTG GCTGACCTGG TCAGTTACAG
 GACAGGGTCG AGAGGTACGA CGGGGTGGAC CGACTGGACC AGTCAATGTC
 LeuSerGln LeuSerMetLeu ProHisLeu AlaAspLeu ValSerTyrSer>
```

FIG. 8C

```
                1010        1020        1030        1040        1050
                  *           *           *           *           *
CATCCAAAAG GTCATTGGCT TTGCTAAGAT GATACCAGGA TTCAGAGACC
GTAGGTTTTC CAGTAACCGA AACGATTCTA CTATGGTCCT AAGTCTCTGG
 IleGlnLys ValIleGly PheAlaLysMet IleProGly PheArgAsp>

      1060        1070        1080        1090        1100
        *           *           *           *           *
TCACCTCTGA GGACCAGATC GTACTGCTGA AGTCAAGTGC CATTGAGGTC
AGTGGAGACT CCTGGTCTAG CATGACGACT TCAGTTCACG GTAACTCCAG
LeuThrSerGlu AspGlnIle ValLeuLeu LysSerSerAla IleGluVal>

      1110        1120        1130        1140        1150
        *           *           *           *           *
ATCATGTTGC GCTCCAATGA GTCCTTCACC ATGGACGACA TGTCCTGGAC
TAGTACAACG CGAGGTTACT CAGGAAGTGG TACCTGCTGT ACAGGACCTG
IleMetLeu ArgSerAsnGlu SerPheThr MetAspAsp MetSerTrpThr>

      1160        1170        1180        1190        1200
        *           *           *           *           *
CTGTGGCAAC CAAGACTACA AGTACCGCGT CAGTGACGTG ACCAAAGCCG
GACACCGTTG GTTCTGATGT TCATGGCGCA GTCACTGCAC TGGTTTCGGC
 CysGlyAsn GlnAspTyr LysTyrArgVal SerAspVal ThrLysAla>

      1210        1220        1230        1240        1250
        *           *           *           *           *
GACACAGCCT GGAGCTGATT GAGCCCCTCA TCAAGTTCCA GGTGGGACTG
CTGTGTCGGA CCTCGACTAA CTCGGGGAGT AGTTCAAGGT CCACCCTGAC
GlyHisSerLeu GluLeuIle GluProLeu IleLysPheGln ValGlyLeu>

      1260        1270        1280        1290        1300
        *           *           *           *           *
AAGAAGCTGA ACTTGCATGA GGAGGAGCAT GTCCTGCTCA TGGCCATCTG
TTCTTCGACT TGAACGTACT CCTCCTCGTA CAGGACGAGT ACCGGTAGAC
LysLysLeu AsnLeuHisGlu GluGluHis ValLeuLeu MetAlaIleCys>

      1310        1320        1330        1340        1350
        *           *           *           *           *
CATCGTCTCC CCAGATCGTC CTGGGGTGCA GGACGCCGCG CTGATTGAGG
GTAGCAGAGG GGTCTAGCAG GACCCCACGT CCTGCGGCGC GACTAACTCC
 IleValSer ProAspArg ProGlyValGln AspAlaAla LeuIleGlu>

      1360        1370        1380        1390        1400
        *           *           *           *           *
CCATCCAGGA CCGCCTGTCC AACACACTGC AGACGTACAT CCGCTGCCGC
GGTAGGTCCT GGCGGACAGG TTGTGTGACG TCTGCATGTA GGCGACGGCG
AlaIleGlnAsp ArgLeuSer AsnThrLeu GlnThrTyrIle ArgCysArg>

      1410        1420        1430        1440        1450
        *           *           *           *           *
CACCCGCCCC CGGGCAGCCA CCTGCTCTAT GCCAAGATGA TCCAGAAGCT
GTGGGCGGGG GCCCGTCGGT GGACGAGATA CGGTTCTACT AGGTCTTCGA
HisProPro ProGlySerHis LeuLeuTyr AlaLysMet IleGlnLysLeu>

      1460        1470        1480        1490        1500
        *           *           *           *           *
AGCCGACCTG CGCAGCCTCA ATGAGGAGCA CTCCAAGCAG TACCGCTGCC
TCGGCTGGAC GCGTCGGAGT TACTCCTCGT GAGGTTCGTC ATGGCGACGG
 AlaAspLeu ArgSerLeu AsnGluGluHis SerLysGln TyrArgCys>
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FIG. 8D

~~120/20~~

```
        1510        1520        1530        1540        1550
          *           *           *           *           *
 TCTCCTTCCA GCCTGAGTGC AGCATGAAGC TAACGCCCCT TGTGCTCGAA
 AGAGGAAGGT CGGACTCACG TCGTACTTCG ATTGCGGGGA ACACGAGCTT
LeuSerPheGln ProGluCys SerMetLys LeuThrProLeu ValLeuGlu>

        1560        1570
          *           *
 GTGTTTGGCA ATGAGATCTC CTGA (SEQ ID NO: 7)
 CACAAACCGT TACTCTAGAG GACT (SEQ ID NO: 20)
 ValPheGly AsnGluIleSer ***> (SEQ ID NO: 12)
```

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FIG. 5C

```
                860       870       880       890       900
                *  *      *  *      *  *      *  *      *  *
CTCCATGCTG CCCCACCTGG CTGACCTGGT CAGTTACAGC ATCCAAAAGG
GAGGTACGAC GGGGTGGACC GACTGGACCA GTCAATGTCG TAGGTTTTCC
 SerMetLeu ProHisLeu AlaAspLeuVal SerTyrSer IleGlnLys>

          910       920       930       940       950
          *  *      *  *      *  *      *  *      *  *
TCATTGGCTT TGCTAAGATG ATACCAGGAT TCAGAGACCT CACCTCTGAG
AGTAACCGAA ACGATTCTAC TATGGTCCTA AGTCTCTGGA GTGGAGACTC
ValIleGlyPhe AlaLysMet IleProGly PheArgAspLeu ThrSerGlu>

          960       970       980       990       1000
          *  *      *  *      *  *      *  *      *  *
GACCAGATCG TACTGCTGAA GTCAAGTGCC ATTGAGGTCA TCATGTTGCG
CTGGTCTAGC ATGACGACTT CAGTTCACGG TAACTCCAGT AGTACAACGC
AspGlnIle ValLeuLeuLys SerSerAla IleGluVal IleMetLeuArg>

          1010      1020      1030      1040      1050
          *  *      *  *      *  *      *  *      *  *
CTCCAATGAG TCCTTCACCA TGGACGACAT GTCCTGGACC TGTGGCAACC
GAGGTTACTC AGGAAGTGGT ACCTGCTGTA CAGGACCTGG ACACCGTTGG
 SerAsnGlu SerPheThr MetAspAspMet SerTrpThr CysGlyAsn>

          1060      1070      1080      1090      1100
          *  *      *  *      *  *      *  *      *  *
 AAGACTACAA GTACCGCGTC AGTGACGTGA CCAAAGCCGG ACACAGCCTG
 TTCTGATGTT CATGGCGCAG TCACTGCACT GGTTTCGGCC TGTGTCGGAC
GlnAspTyrLys TyrArgVal SerAspVal ThrLysAlaGly HisSerLeu>

          1110      1120      1130      1140      1150
          *  *      *  *      *  *      *  *      *  *
 GAGCTGATTG AGCCCCTCAT CAAGTTCCAG GTGGGACTGA AGAAGCTGAA
 CTCGACTAAC TCGGGGAGTA GTTCAAGGTC CACCCTGACT TCTTCGACTT
 GluLeuIle GluProLeuIle LysPheGln ValGlyLeu LysLysLeuAsn>

          1160      1170      1180      1190      1200
          *  *      *  *      *  *      *  *      *  *
 CTTGCATGAG GAGGAGCATG TCCTGCTCAT GGCCATCTGC ATCGTCTCCC
 GAACGTACTC CTCCTCGTAC AGGACGAGTA CCGGTAGACG TAGCAGAGGG
  LeuHisGlu GluGluHis ValLeuLeuMet AlaIleCys IleValSer>

          1210      1220      1230      1240      1250
          *  *      *  *      *  *      *  *      *  *
 CAGATCGTCC TGGGGTGCAG GACGCCGCGC TGATTGAGGC CATCCAGGAC
 GTCTAGCAGG ACCCCACGTC CTGCGGCGCG ACTAACTCCG GTAGGTCCTG
 ProAspArgPro GlyValGln AspAlaAla LeuIleGluAla IleGlnAsp>

          1260      1270      1280      1290      1300
          *  *      *  *      *  *      *  *      *  *
 CGCCTGTCCA ACACACTGCA GACGTACATC CGCTGCCGCC ACCCGCCCCC
 GCGGACAGGT TGTGTGACGT CTGCATGTAG GCGACGGCGG TGGGCGGGGG
 ArgLeuSer AsnThrLeuGln ThrTyrIle ArgCysArg HisProProPro>
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FIG. 5D

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```
      1310        1320        1330        1340        1350
    *    *      *    *      *    *      *    *      *    *
GGGCAGCCAC CTGCTCTATG CCAAGATGAT CCAGAAGCTA GCCGACCTGC
CCCGTCGGTG GACGAGATAC GGTTCTACTA GGTCTTCGAT CGGCTGGACG
 GlySerHis LeuLeuTyr AlaLysMetIle GlnLysLeu AlaAspLeu>

      1360        1370        1380        1390        1400
    *    *      *    *      *    *      *    *      *    *
GCAGCCTCAA TGAGGAGCAC TCCAAGCAGT ACCGCTGCCT CTCCTTCCAG
CGTCGGAGTT ACTCCTCGTG AGGTTCGTCA TGGCGACGGA GAGGAAGGTC
ArgSerLeuAsn GluGluHis SerLysGln TyrArgCysLeu SerPheGln>

      1410        1420        1430        1440        1450
    *    *      *    *      *    *      *    *      *    *
CCTGAGTGCA GCATGAAGCT AACGCCCCTT GTGCTCGAAG TGTTTGGCAA
GGACTCACGT CGTACTTCGA TTGCGGGGAA CACGAGCTTC ACAAACCGTT
ProGluCys SerMetLysLeu ThrProLeu ValLeuGlu ValPheGlyAsn>

      1460
    *    *
TGAGATCTCC TGA (SEQ ID NO:2)
ACTCTAGAGG ACT (SEQ ID NO:17)
 GluIleSer ***> (SEQ ID NO:9)
```

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FIG. 6A

~~FIGURE 6~~ TRANSCRIPT 9

(Sequence Range: 1 to 1382)

```
        10         20         30         40         50
    *   *    *     *    *     *    *     *    *     *    *
GTTTCCTTCT TCTGTCGGGG CGCCTTGGCA TGGAGTGGAG GAATAAGAAA
CAAAGGAAGA AGACAGCCCC GCGGAACCGT ACCTCACCTC CTTATTCTTT
                                  MetGluTrpArg AsnLysLys>

        60         70         80         90         100
    *   *    *     *    *     *    *     *    *     *    *
AGGAGCGATT GGCTGTCGAT GGTGCTCAGA ACTGCTGGAG TGGAGGGGAT
TCCTCGCTAA CCGACAGCTA CCACGAGTCT TGACGACCTC ACCTCCCCTA
ArgSerAsp TrpLeuSerMet ValLeuArg ThrAlaGly ValGluGlyMet>

        110        120        130        140        150
    *   *    *     *    *     *    *     *    *     *    *
GGAGGCAATG GCGGCCAGCA CTTCCCTGCC TGACCCTGGA GACTTTGACC
CCTCCGTTAC CGCCGGTCGT GAAGGGACGG ACTGGGACCT CTGAAACTGG
 GluAlaMet AlaAlaSer ThrSerLeuPro AspProGly AspPheAsp>

        160        170        180        190        200
    *   *    *     *    *     *    *     *    *     *    *
GGAACGTGCC CCGGATCTGT GGGGTGTGTG GAGACCGAGC CACTGGCTTT
CCTTGCACGG GGCCTAGACA CCCCACACAC CTCTGGCTCG GTGACCGAAA
ArgAsnValPro ArgIleCys GlyValCys GlyAspArgAla ThrGlyPhe>

        210        220        230        240        250
    *   *    *     *    *     *    *     *    *     *    *
CACTTCAATG CTATGACCTG TGAAGGCTGC AAAGGCTTCT TCAGGCGAAG
GTGAAGTTAC GATACTGGAC ACTTCCGACG TTTCCGAAGA AGTCCGCTTC
HisPheAsn AlaMetThrCys GluGlyCys LysGlyPhe PheArgArgSer>

        260        270        280        290        300
    *   *    *     *    *     *    *     *    *     *    *
CATGAAGCGG AAGGCACTAT TCACCTGCCC CTTCAACGGG GACTGCCGCA
GTACTTCGCC TTCCGTGATA AGTGGACGGG GAAGTTGCCC CTGACGGCGT
 MetLysArg LysAlaLeu PheThrCysPro PheAsnGly AspCysArg>

        310        320        330        340        350
    *   *    *     *    *     *    *     *    *     *    *
TCACCAAGGA CAACCGACGC CACTGCCAGG CCTGCCGGCT CAAACGCTGT
AGTGGTTCCT GTTGGCTGCG GTGACGGTCC GGACGGCCGA GTTTGCGACA
IleThrLysAsp AsnArgArg HisCysGln AlaCysArgLeu LysArgCys>

        360        370        380        390        400
    *   *    *     *    *     *    *     *    *     *    *
GTGGACATCG GCATGATGAA GGAGTTCATT CTGACAGATG AGGAAGTGCA
CACCTGTAGC CGTACTACTT CCTCAAGTAA GACTGTCTAC TCCTTCACGT
ValAspIle GlyMetMetLys GluPheIle LeuThrAsp GluGluValGln>
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FIG. 6B


```
       410        420        430        440        450
    *    *     *    *     *    *     *    *     *    *
GAGGAAGCGG GAGATGATCC TGAAGCGGAA GGAGGAGGAG GCCTTGAAGG
CTCCTTCGCC CTCTACTAGG ACTTCGCCTT CCTCCTCCTC CGGAACTTCC
 ArgLysArg GluMetIle LeuLysArgLys GluGluGlu AlaLeuLys>

       460        470        480        490        500
    *    *     *    *     *    *     *    *     *    *
ACAGTCTGCG GCCCAAGCTG TCTGAGGAGC AGCAGCGCAT CATTGCCATA
TGTCAGACGC CGGGTTCGAC AGACTCCTCG TCGTCGCGTA GTAACGGTAT
AspSerLeuArg ProLysLeu SerGluGlu GlnGlnArgIle IleAlaIle>

       510        520        530        540        550
    *    *     *    *     *    *     *    *     *    *
CTGCTGGACG CCCACCATAA GACCTACGAC CCCACCTACT CCGACTTCTG
GACGACCTGC GGGTGGTATT CTGGATGCTG GGGTGGATGA GGCTGAAGAC
LeuLeuAsp AlaHisHisLys ThrTyrAsp ProThrTyr SerAspPheCys>

       560        570        580        590        600
    *    *     *    *     *    *     *    *     *    *
CCAGTTCCGG CCTCCAGTTC GTGTGAATGA TGGTGGAGGG AGCCATCCTT
GGTCAAGGCC GGAGGTCAAG CACACTTACT ACCACCTCCC TCGGTAGGAA
 GlnPheArg ProProVal ArgValAsnAsp GlyGlyGly SerHisPro>

       610        620        630        640        650
    *    *     *    *     *    *     *    *     *    *
CCAGGCCCAA CTCCAGACAC ACTCCCAGCT TCTCTGGGGA CTCCTCCTCC
GGTCCGGGTT GAGGTCTGTG TGAGGGTCGA AGAGACCCCT GAGGAGGAGG
SerArgProAsn SerArgHis ThrProSer PheSerGlyAsp SerSerSer>

       660        670        680        690        700
    *    *     *    *     *    *     *    *     *    *
TCCTGCTCAG ATCACTGTAT CACCTCTTCA GACATGATGG ACTCGTCCAG
AGGACGAGTC TAGTGACATA GTGGAGAAGT CTGTACTACC TGAGCAGGTC
SerCysSer AspHisCysIle ThrSerSer AspMetMet AspSerSerSer>

       710        720        730        740        750
    *    *     *    *     *    *     *    *     *    *
CTTCTCCAAT CTGGATCTGA GTGAAGAAGA TTCAGATGAC CCTTCTGTGA
GAAGAGGTTA GACCTAGACT CACTTCTTCT AAGTCTACTG GGAAGACACT
 PheSerAsn LeuAspLeu SerGluGluAsp SerAspAsp ProSerVal>

       760        770        780        790        800
    *    *     *    *     *    *     *    *     *    *
CCCTAGAGCT GTCCCAGCTC TCCATGCTGC CCCACCTGGC TGACCTGGTC
GGGATCTCGA CAGGGTCGAG AGGTACGACG GGGTGGACCG ACTGGACCAG
ThrLeuGluLeu SerGlnLeu SerMetLeu ProHisLeuAla AspLeuVal>

       810        820        830        840        850
    *    *     *    *     *    *     *    *     *    *
AGTTACAGCA TCCAAAAGGT CATTGGCTTT GCTAAGATGA TACCAGGATT
TCAATGTCGT AGGTTTTCCA GTAACCGAAA CGATTCTACT ATGGTCCTAA
SerTyrSer IleGlnLysVal IleGlyPhe AlaLysMet IleProGlyPhe>
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       860        870        880        890        900
    *    *     *    *     *    *     *    *     *    *
CAGAGACCTC ACCTCTGAGG ACCAGATCGT ACTGCTGAAG TCAAGTGCCA
GTCTCTGGAG TGGAGACTCC TGGTCTAGCA TGACGACTTC AGTTCACGGT
 ArgAspLeu ThrSerGlu AspGlnIleVal LeuLeuLys SerSerAla>

       910        920        930        940        950
    *    *     *    *     *    *     *    *     *    *
TTGAGGTCAT CATGTTGCGC TCCAATGAGT CCTTCACCAT GGACGACATG
AACTCCAGTA GTACAACGCG AGGTTACTCA GGAAGTGGTA CCTGCTGTAC
IleGluValIle MetLeuArg SerAsnGlu SerPheThrMet AspAspMet>

       960        970        980        990       1000
    *    *     *    *     *    *     *    *     *    *
TCCTGGACCT GTGGCAACCA AGACTACAAG TACCGCGTCA GTGACGTGAC
AGGACCTGGA CACCGTTGGT TCTGATGTTC ATGGCGCAGT CACTGCACTG
SerTrpThr CysGlyAsnGln AspTyrLys TyrArgVal SerAspValThr>

      1010       1020       1030       1040       1050
    *    *     *    *     *    *     *    *     *    *
CAAAGCCGGA CACAGCCTGG AGCTGATTGA GCCCCTCATC AAGTTCCAGG
GTTTCGGCCT GTGTCGGACC TCGACTAACT CGGGGAGTAG TTCAAGGTCC
 LysAlaGly HisSerLeu GluLeuIleGlu ProLeuIle LysPheGln>

      1060       1070       1080       1090       1100
    *    *     *    *     *    *     *    *     *    *
TGGGACTGAA GAAGCTGAAC TTGCATGAGG AGGAGCATGT CCTGCTCATG
ACCCTGACTT CTTCGACTTG AACGTACTCC TCCTCGTACA GGACGAGTAC
ValGlyLeuLys LysLeuAsn LeuHisGlu GluGluHisVal LeuLeuMet>

      1110       1120       1130       1140       1150
    *    *     *    *     *    *     *    *     *    *
GCCATCTGCA TCGTCTCCCC AGATCGTCCT GGGGTGCAGG ACGCCGCGCT
CGGTAGACGT AGCAGAGGGG TCTAGCAGGA CCCCACGTCC TGCGGCGCGA
AlaIleCys IleValSerPro AspArgPro GlyValGln AspAlaAlaLeu>

      1160       1170       1180       1190       1200
    *    *     *    *     *    *     *    *     *    *
GATTGAGGCC ATCCAGGACC GCCTGTCCAA CACACTGCAG ACGTACATCC
CTAACTCCGG TAGGTCCTGG CGGACAGGTT GTGTGACGTC TGCATGTAGG
 IleGluAla IleGlnAsp ArgLeuSerAsn ThrLeuGln ThrTyrIle>

      1210       1220       1230       1240       1250
    *    *     *    *     *    *     *    *     *    *
GCTGCCGCCA CCCGCCCCCG GGCAGCCACC TGCTCTATGC CAAGATGATC
CGACGGCGGT GGGCGGGGGC CCGTCGGTGG ACGAGATACG GTTCTACTAG
ArgCysArgHis ProProPro GlySerHis LeuLeuTyrAla LysMetIle>

      1260       1270       1280       1290       1300
    *    *     *    *     *    *     *    *     *    *
CAGAAGCTAG CCGACCTGCG CAGCCTCAAT GAGGAGCACT CCAAGCAGTA
GTCTTCGATC GGCTGGACGC GTCGGAGTTA CTCCTCGTGA GGTTCGTCAT
GlnLysLeu AlaAspLeuArg SerLeuAsn GluGluHis SerLysGlnTyr>
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FIG. 6D


```
      1310        1320        1330        1340        1350
    *    *      *    *      *    *      *    *      *    *
CCGCTGCCTC TCCTTCCAGC CTGAGTGCAG CATGAAGCTA ACGCCCCTTG
GGCGACGGAG AGGAAGGTCG GACTCACGTC GTACTTCGAT TGCGGGGAAC
 ArgCysLeu SerPheGln ProGluCysSer MetLysLeu ThrProLeu>

      1360        1370        1380
    *    *      *    *      *    *
TGCTCGAAGT GTTTGGCAAT GAGATCTCCT GA (SEQ ID NO: 3)
ACGAGCTTCA CAAACCGTTA CTCTAGAGGA CT (SEQ ID NO: 18)
ValLeuGluVal PheGlyAsn GluIleSer ***> (SEQ ID NO: 10)
```